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Barany et al.

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[54] **THERMOSTABLE LIGASE MEDIATED DNA AMPLIFICATION SYSTEM FOR THE DETECTION OF GENETIC DISEASES**

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[21] Appl. No.: **08/946,458**

[22] Filed: **Oct. 7, 1997**

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[62] Division of application No. 08/462,221, Jun. 5, 1995, Pat. No. 5,830,711, which is a continuation of application No. 08/343,785, Nov. 22, 1994, Pat. No. 5,494,810, which is a continuation of application No. 07/971,095, Nov. 2, 1992, abandoned, which is a continuation-in-part of application No. 07/518,447, May 3, 1990, abandoned.

[51] **Int. Cl.**^{7} **C12Q 1/68**; C07H 19/00; C07H 21/02; C07H 21/04

[52] **U.S. Cl.** **536/22.1**; 435/6; 435/91.1; 435/440; 435/455; 435/471; 536/23.1; 536/23.2; 536/23.4; 536/23.5

[58] **Field of Search** 536/22.1, 23.1, 536/23.2, 23.4, 23.5; 435/6, 91.1, 440, 455, 471

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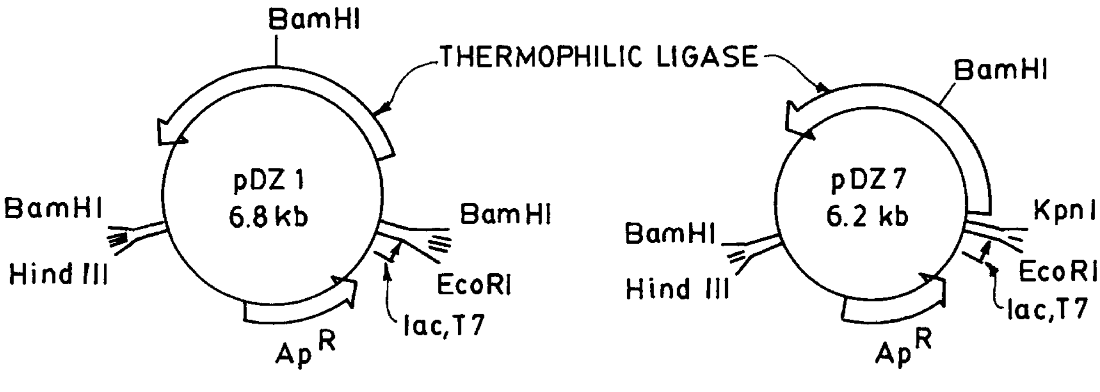
[57] **ABSTRACT**

The present invention relates to the cloning of the gene of a thermophilic DNA ligase, from *Thermus aquaticus* strain HB8, and the use of this ligase for the detection of specific sequences of nucleotides in a variety of nucleic acid samples, and more particularly in those samples containing a DNA sequence characterized by a difference in the nucleic acid sequence from a standard sequence including single nucleic acid base pair changes, deletions, insertions or translocations.

19 Claims, 8 Drawing Sheets



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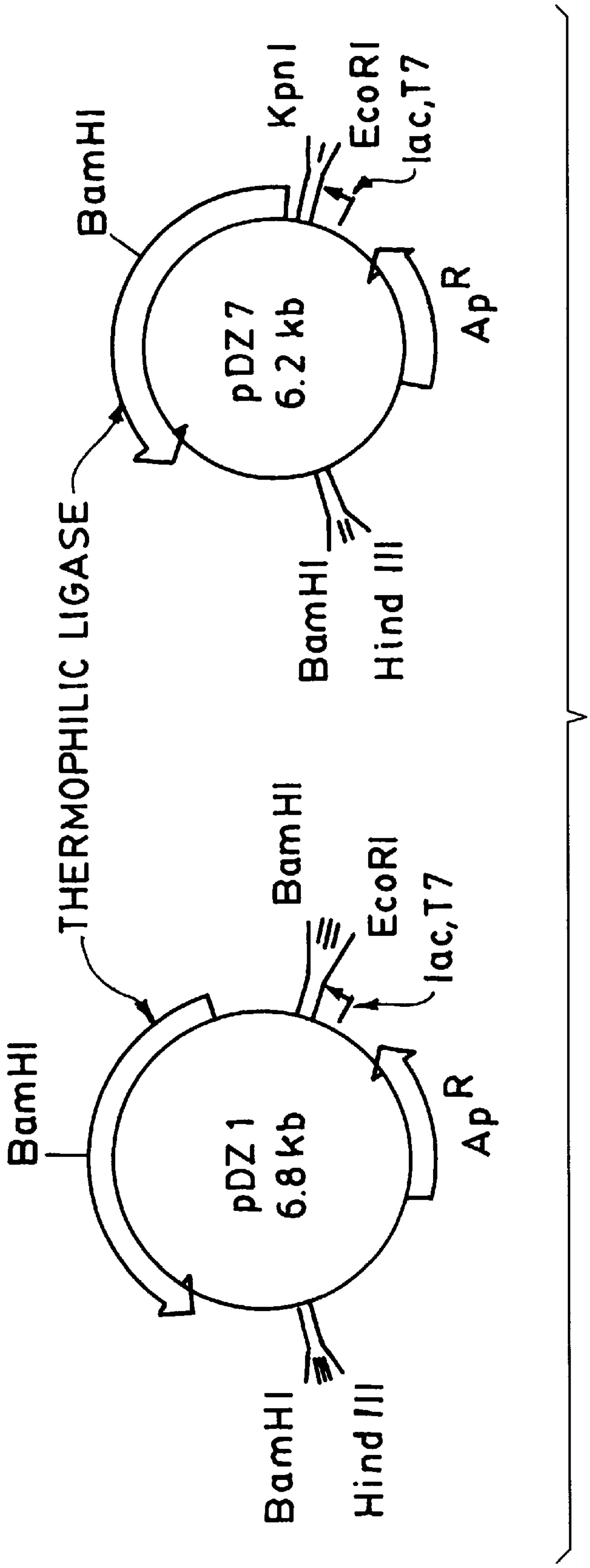
BamHI
pDZ1
6.8 kb
Ap^R
BamHI
EcoRI
lac,T7
BamHI
Hind III
THERMOPHILIC LIGASE
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KpnI
EcoRI
lac,T7
pDZ7
6.2 kb
Ap^R
BamHI
Hind III

FIG. 1

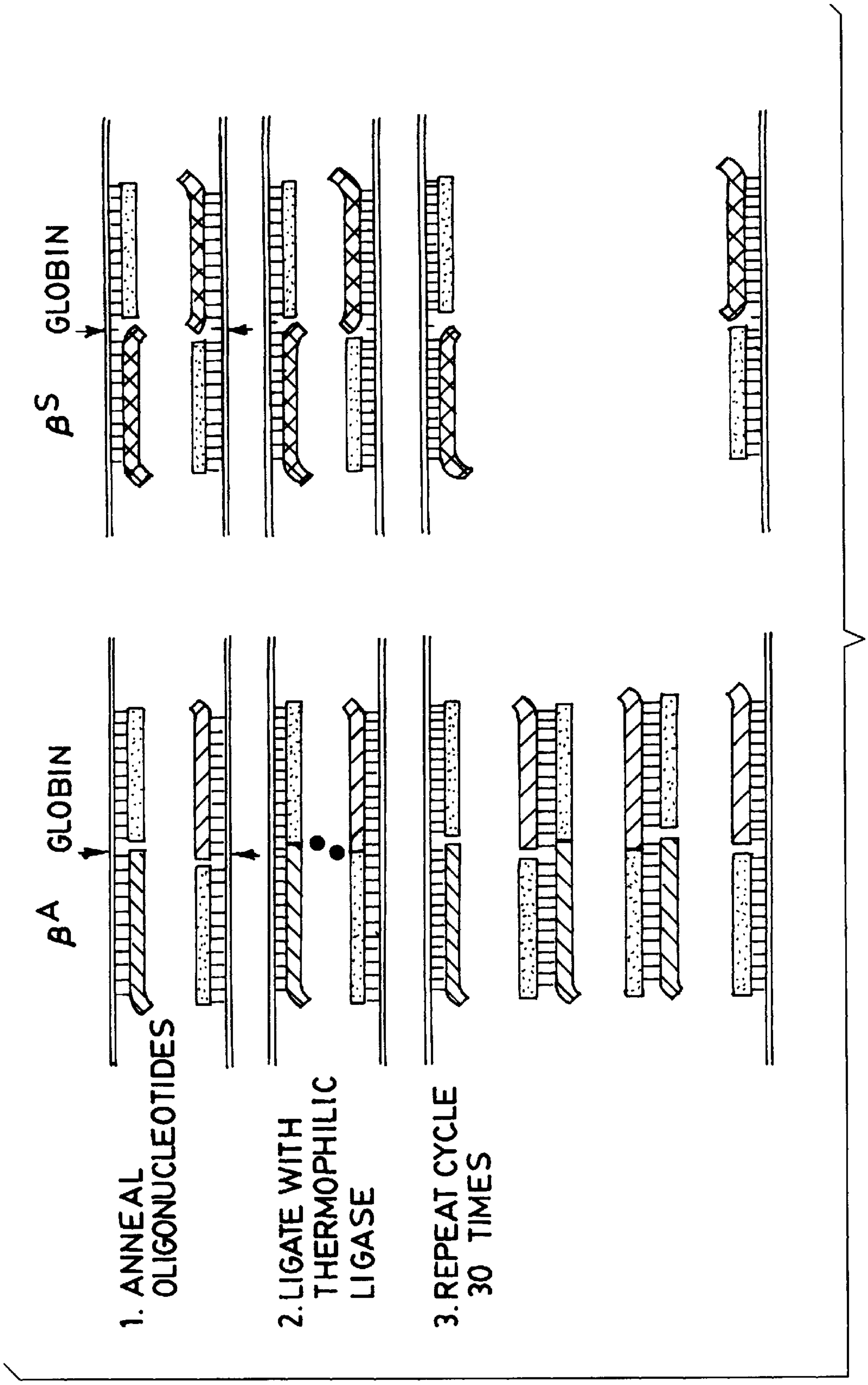
β^A GLOBIN
β^S GLOBIN
1. ANNEAL OLIGONUCLEOTIDES
2. LIGATE WITH THERMOPHILIC LIGASE
3. REPEAT CYCLE 30 TIMES

FIG. 2

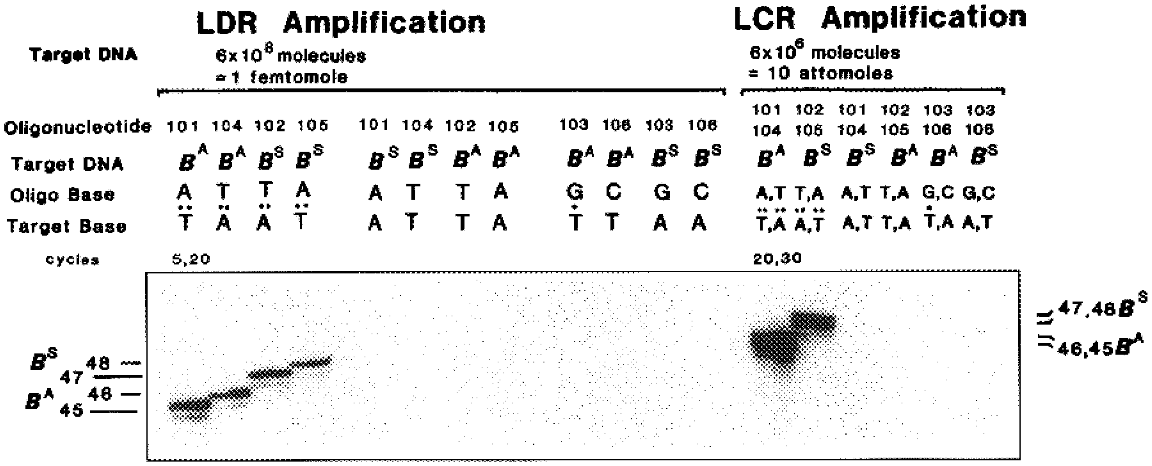
LDR Amplification
LCR Amplification
Target DNA
6x10^8 molecules
≈ 1 femtomole
6x10^6 molecules
≈ 10 attomoles
Oligonucleotide 101 104 102 105 101 104 102 105 103 106 103 106
101 102 101 102 103 103
104 105 104 105 106 106
Target DNA B^A B^A B^S B^S B^S B^S B^A B^A B^A B^A B^S B^S B^A B^S B^S B^A B^A B^S
Oligo Base A T T A A T T A G C G C A,T T,A A,T T,A G,C G,C
Target Base T A A T A T T A T T A A T,A A,T A,T T,A T,A A,T
cycles 5,20
20,30
B^S 47 48
B^A 45 46
47,48 B^S
46,45 B^A

FIG. 3

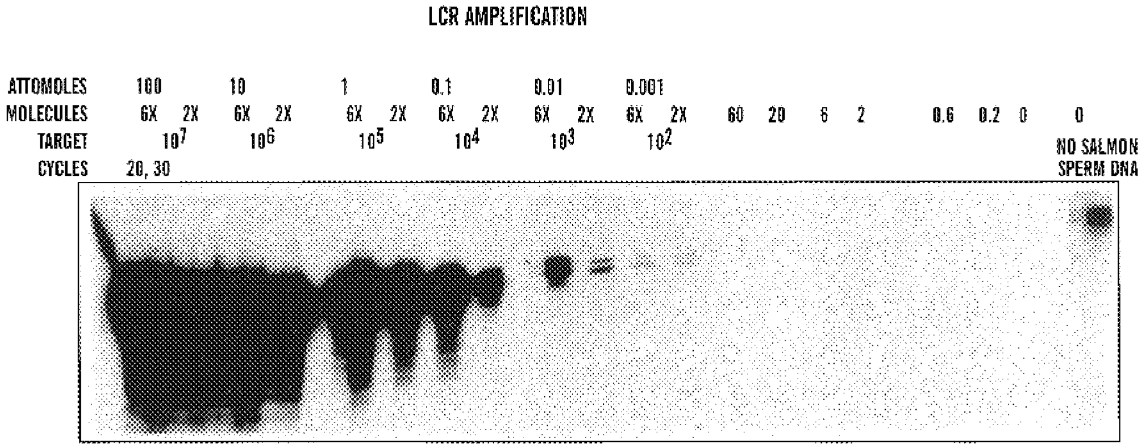
LCR AMPLIFICATION
ATTOMOLES 100 10 1 0.1 0.01 0.001
MOLECULES 6X 2X 6X 2X 6X 2X 6X 2X 6X 2X 6X 2X 60 20 6 2 0.6 0.2 0 0
TARGET 10^7 10^6 10^5 10^4 10^3 10^2
CYCLES 20, 30
NO SALMON SPERM DNA

FIG. 4

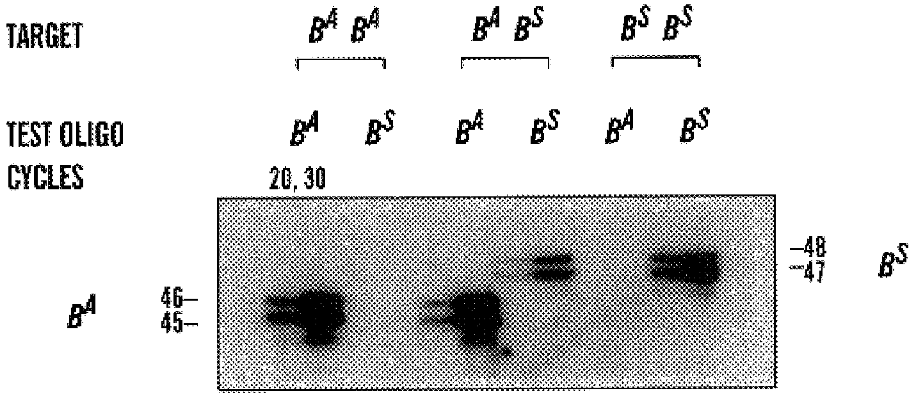
TARGET
B^A B^A
B^A B^S
B^S B^S
TEST OLIGO
B^A B^S B^A B^S B^A B^S
CYCLES
20, 30
B^A
46–
45–
–48
–47
B^S

FIG. 5

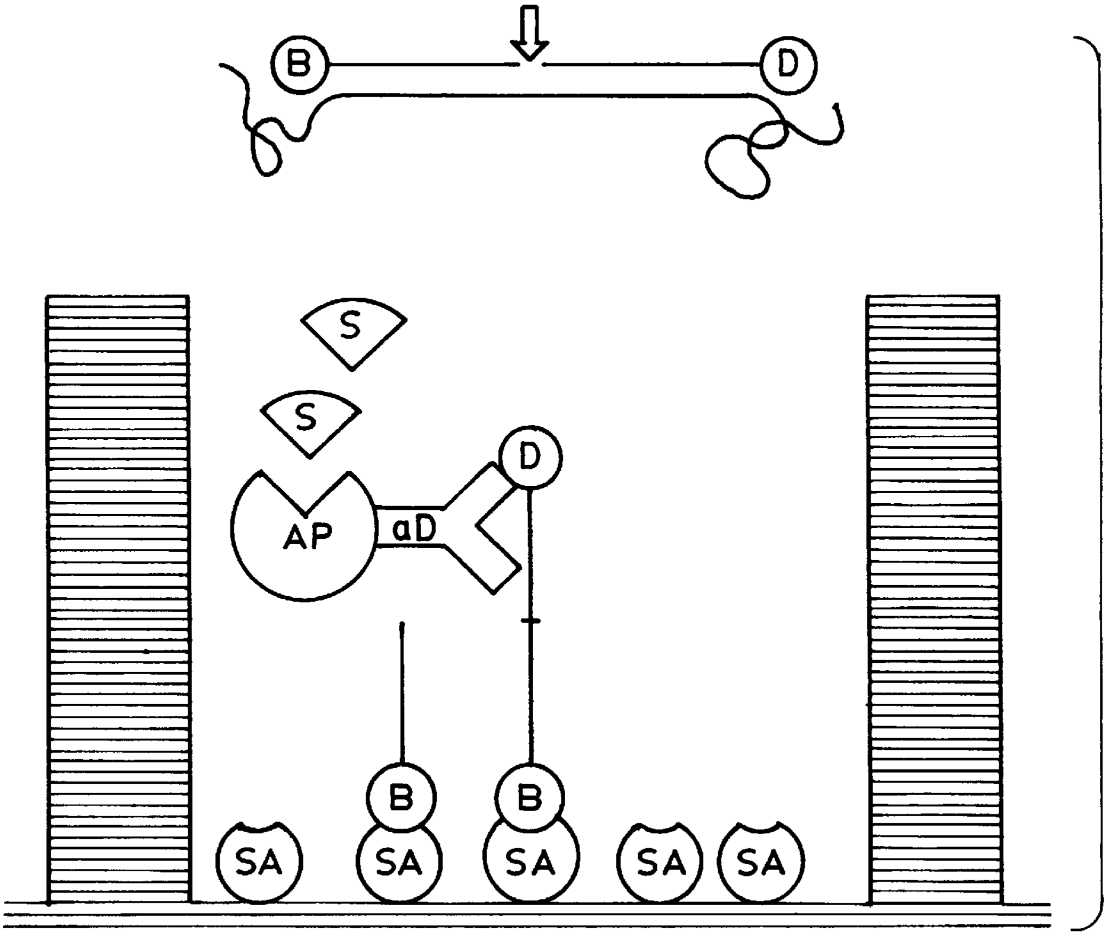

FIG. 6

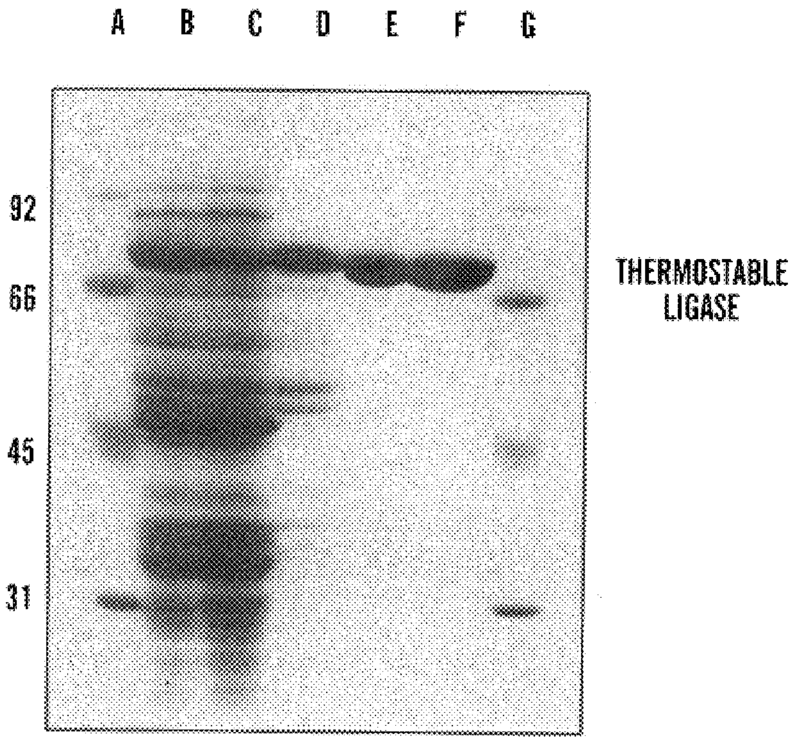
A
B
C
D
E
F
G
92
66
45
31
THERMOSTABLE
LIGASE

FIG. 7

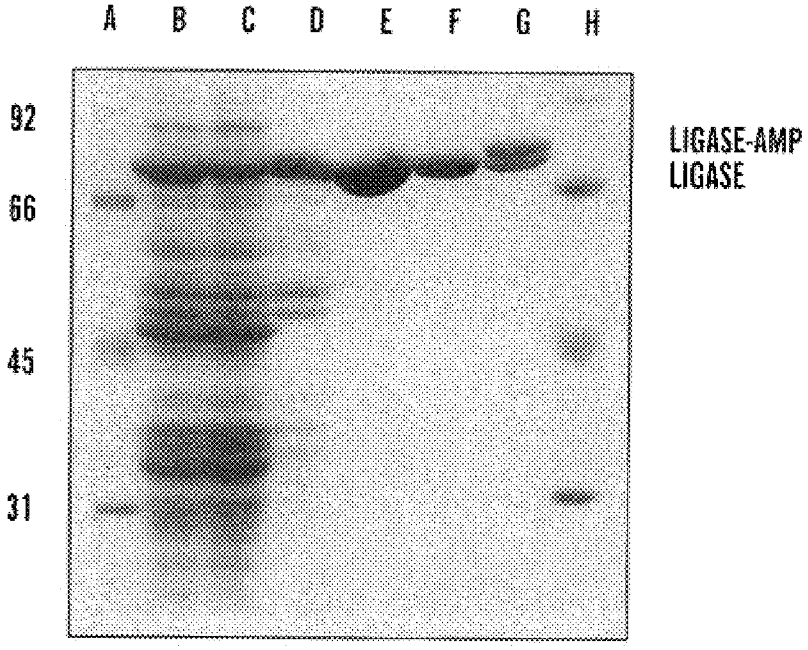
A
B
C
D
E
F
G
H
92
66
45
31
LIGASE-AMP
LIGASE

FIG. 8

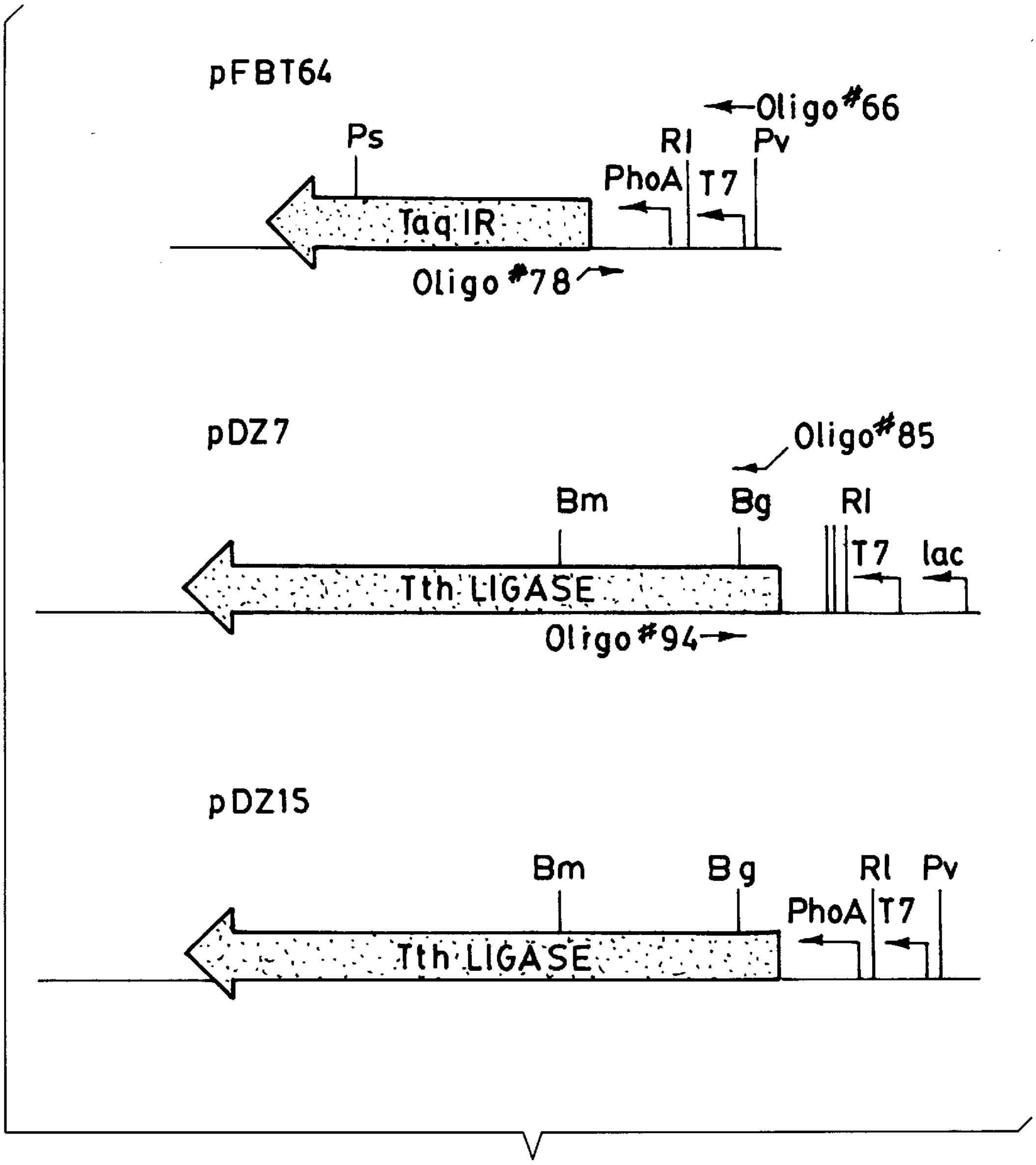
pFBT64
Oligo #66
Ps
RI
Pv
PhoA
T7
Taq IR
Oligo #78
pDZ7
Oligo #85
Bm
Bg
RI
T7
lac
Tth LIGASE
Oligo #94
pDZ15
Bm
Bg
RI
Pv
PhoA
T7
Tth LIGASE

FIG. 9

THERMOSTABLE LIGASE MEDIATED DNA AMPLIFICATION SYSTEM FOR THE DETECTION OF GENETIC DISEASES

This is a division of application Ser. No. 08/462,221, filed on Jun. 5, 1995, now U.S. Pat. No. 5,830,711 which is a continuation of application Ser. No. 08/343,785, filed Nov. 22, 1994, now U.S. Pat. No. 5,494,810, which is a continuation of application Ser. No. 07/971,095, filed Nov. 2, 1992, now abandoned, which is a continuation-in-part of application Ser. No. 07/518,447, filed May 3, 1990, now abandoned.

More than 2,000 conditions have been identified as single-gene defects for which the risk of producing affected offspring can be mathematically predicted. Among these conditions in man include Huntington's chorea, cystic fibrosis, alpha$_1$ antitrypsin deficiency, muscular dystrophy, Hunter's syndrome, Lesch-Nyhan syndrome, Down's syndrome, Tay-Sachs disease, hemophilias, phenylketonuria, thalasemias, and sickle-cell anemia.

Three important techniques have been developed recently for directly detecting these single nucleic acid base pair changes, deletions, insertions, translocations or other mutations. However, two of these techniques cannot be easily automated. In the first such technique, the presence or absence of the mutation in a patient's clinical sample is detected by analysis of a restriction digest of the patient's DNA using Southern blotting [see Journal of Molecular Biology 98:503 (1975)]. However, the Southern blotting technique cannot be used for genetic diseases where the mutation does not alter a restriction site as, for example in alpha$_1$ antitrypsin deficiency. The second technique is by the use of DNA probes which involves the synthesis of an oligonucleotide of about 19 base pairs that is complementary to the normal DNA sequence around the mutation site. The probe is labelled and used to distinguish normal from mutant genes by raising the stringency of hybridization to a level which the probe will hybridize stably to the normal gene, but not to the mutant gene with which it has a single base pair mismatch [see Proc. Natl. Acad. Sci. USA 80:278 (1983)]. The original method has been modified by immobilizing the oligonucleotide and probing with a labelled PCR amplified sample. In this modification, the sample is allowed to hybridize to an immobilized oligonucleotide and then washed off by raising the stringency of hybridization as described above [see Proc. Natl, Acad. Sci. USA 86:6230 (1989)]. Other methods have been developed which use fluorescent PCR primers to specifically amplify only one mutation or allele [see Proc. Natl. Acad. Sci. USA 86:9178 (1989)]. This method requires the separation of products from primers by spin columns or gel electrophoresis and hence is not amenable to large scale automation. The third technique utilizes the presence of both diagnostic and contiguous probes under conditions wherein the diagnostic probe remains substantially covalently bound to the contiguous probe only in the case wherein the sample nucleic acid contains the exact target sequence. In addition, the diagnostic oligonucleotide probe may contain a "hook" (for example, a biotinylated oligonucleotide) which is captured (for example, by streptavidin) as a means of increasing the efficiency of the technique, and the contiguous probe may contain a detectable moiety or label [see Science 241:1077 (1988) and U.S. Pat. No. 4,883,750].

Although it is not always necessary, the detection of single base pair mutations in DNA is usually preceded by techniques to increase or amplify the amount of DNA sample material. A number of techniques exist to perform nucleic acid amplification, among which are: (1) polymerase chain reaction which can amplify DNA a million fold from a single copy in a matter of hours using Taq polymerase and running 20 to 30 reaction cycles on a temperature cycling instrument [see Science 239:487 (1988), and U.S. Pat. Nos. 4,683,195, 4,683,202, and 4,800,159]; (2) self-sustained sequence replication or 3SR can amplify DNA or RNA 10 million fold from a single copy in less than an hour using reverse transcriptase, T7 RNA polymerase, and RNase H under isothermal conditions at 37° C. [see Proc. Natl. Acad. Sci. USA 87:1874 (1990)]; and (3) Q Beta Replicase can replicate a few thousand RNA molecules containing a special 300 bp recognition sequence a billion fold in 30 minutes. Additional techniques are available, and one, the ligase chain reaction, is discussed in the following description of the cloned thermophilic ligase according to the present invention.

In addition to various genetic diseases which may be diagnosed utilizing the present invention, various infectious diseases can be diagnosed by the presence in a clinical sample of a specific DNA sequence characteristic of the causative microorganism. These include bacteria, viruses, and parasites. In such procedures, a relatively small number of pathogenic organisms may be present in a clinical sample from an infected patient and the DNA extracted from these organisms may constitute only a very small fraction of the total DNA in the sample. However, specific amplification of suspected pathogen-specific sequences prior to immobilization and detection by hybridization of the DNA samples should greatly improve the sensitivity and specificity of traditional procedures. In addition, amplification is particularly useful if such an analysis is to be done on a small sample using nonradioactive detection techniques which may be inherently insensitive, or where radioactive techniques are employed, but where rapid detection is desirable.

Although techniques such as these are available, the search for other techniques for determining single base pair mutations continues. The present invention, that is DNA amplification and/or detection by a ligase detection reaction (LDR) or ligase chain reaction (LCR) utilizing the thermophilic DNA ligase from *Thermus aquaticus* to detect a target DNA sequence is part of that continuing effort.

Although other techniques utilizing *E. coli* or T4 DNA ligase for DNA amplification have been attempted, these have been found to be unacceptable because of a high background "noise" levels (after as few as 10 cycles), a condition which does not exist in the ligase chain reaction according to the present invention.

DNA amplification and/or detection has also been attempted utilizing specific ligases. For example, a ligase amplification reaction has been reported [see Gene 76:245 (1989)] that can amplify DNA starting with 500,000 copies in 95 hours, using 75 cycles and replenishing the T4 DNA ligase used after each cycle. However, this reported technique is slow and requires the addition of fresh T4 ligase at each step, both of which requirements make this reported technique unacceptable for automation. The ligase chain reaction according to the present invention allows for amplification of DNA from 200 copies in 3 hours using 30 cycles and does not require the addition of ligase following each cycle.

Throughout the following description of the present invention, terminology specific to the technology field will be used. In order to avoid any misunderstandings as to what is being referenced, and to provide the reader with a clear understanding of what is being described, the following definitions will be used:

"Amplification" refers to the increase in the number of copies of a particular nucleic acid fragment resulting either from an enzymatic chain reaction (such as a polymerase chain reaction, a ligase chain reaction, or a self-sustained sequence replication). or from the replication of the vector into which it has been cloned.

"Blunt end ligation" refers to the covalent linkage of two ends of DNA that are completely flush, i.e. have no cohesive end overhangs.

"Cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" includes the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content due to deliberate or inadvertent mutations. However, all mutant progeny having the same functionality as screened for in the originally transformed cell are included.

"Clone" refers to a group of genetically identical molecules, cells or organisms asexually descended from a common ancestor. "Cloning" is the process of propagating such identical molecules, cells or organisms. Recombinant DNA techniques make it possible to clone individual genes; this is referred to as "molecular cloning".

"Covalently attaching" refers to forming a covalent chemical bond between two substances.

"Cycle" refers to a single melting and cooling of DNA. For example, at very high temperatures such as 94° C., virtually all double stranded DNA (independent of length) unwinds and melts. If one cools the temperature (to 45–65° C.) in the presence of complementary oligonucleotides, they can hybridize to the correct sequences of the unwound melted DNA. DNA that has been melted and cooled in the presence of complementary oligonucleotides is now a substrate for the DNA ligase reaction. See "T_m".

"Diagnostic portion" refers to that portion of the target sequence which contains the nucleotide change, the presence or absence of which is to be detected. "Contiguous portion" refers to a sequence of DNA which is a continuation of the nucleotide sequence of that portion of the sequence chosen as diagnostic. The continuation can be in either direction.

It will be recognized, based on the following description, that the precise position of the selected oligonucleotide containing the diagnostic portion is arbitrary, except that it must contain the nucleotide(s) which differentiate the presence or absence of the target sequence at one of its ends. Thus, the oligonucleotide containing the contiguous portion continues the sequence of this arbitrarily chosen oligonucleotide containing the diagnostic portion such that the diagnostic nucleotide(s) is at the junction of the two oligonucleotides.

"Endonuclease" refers to an enzyme (e.g., restriction endonuclease, DNase **1**) that cuts DNA at sites within the molecule.

"Expression system" refers to DNA sequences containing a desired coding sequence and control sequence in operable linkage in such a manner that hosts transformed with these sequences are capable of producing the encoded proteins. In order to effect transformation, the expression system may be included on a vector, or the transformed vector DNA may also be integrated into the host chromosome.

"Gene" refers to a DNA sequence which encodes a recoverable bioactive polypeptide or precursor. The polypeptide can be encoded by a full-length gene sequence or any portion of the coding sequence so long as the enzymatic activity is retained.

"Gene library" or "library" refers to a collection of randomly-cloned fragments that encompass substantially the entire genome of a given species. This is also referred to as a clone bank or shotgun collection.

"Genome" refers to the entire DNA of an organism.

"Hook" refers to a modification of a probe that enables the user to rapidly and conveniently isolate probes containing this modification by "catching" the hook. The interaction between hook and catching mechanism can be, for example, covalent bonding or ligand/receptor binding of sufficient affinity. Such hooks may include antigens which can be recovered by antibody, biotin which can be recovered by avidin or streptavidin, specific DNA sequences which can be recovered by complementary nucleic acid, or DNA binding proteins (repressors), and specific reactive chemical functionalities which can be recovered by other appropriate reactive groups.

"Hybridization" and "binding" in the context of probes and denatured melted DNA are used interchangeably. Probes which are hybridized or bound to denatured DNA are base paired or "aggregated" to complementary sequences in the polynucleotide. Whether or not a particular probe remains base paired or aggregated with the polynucleotide depends on the degree of complementarity, the length of the probe, and the stringency of the binding conditions. The higher the stringency, the higher must be the degree of complementarity, and/or the longer the probe.

"Klenow fragment" refers to a 76,000 dalton polypeptide obtained by partial proteolytic digestion of DNA polymerase **1**. This enzyme possesses the 5'→3' polymerase and 3'→5' exonuclease activities, but not the 5'→3' exonuclease activity of DNA polymerase **1**.

"Label" refers to a modification to the probe nucleic acid which enables the user to identify the labelled nucleic acid in the presence of unlabelled nucleic acid. Most commonly, this is the replacement of one or more atoms with radioactive isotopes. However, other labels may be substituted for the isotopes as, for example, covalently attached chromophores, fluorescent moieties, enzymes, antigens, groups with specific reactivity, chemiluminescent moieties, and electrochemically detectable moieties.

"Ligase" refers to an enzyme which catalyses the formation of a phosphodiester bond at the site of a single-stranded break in duplex DNA. The ligase enzyme also catalyses the covalent linkage of duplex DNA; blunt end to blunt end, or one cohesive end to another complementary cohesive end.

"Ligase Chain Reaction (LCR)" refers to the amplification of a oligonucleotide ligation product. For example, if oligonucleotides are designed such that the DNA products of one cycle can become the DNA substrates of the next cycle, repeating such cycles will cause an exponential amplification of the DNA (a "chain reaction"). As a thermophilic ligase enzyme is capable of remaining active during many DNA melting and cooling cycles, this allows a DNA amplification to occur rapidly and automatically in a single reaction vessel subject to many thermal cycles in which the oligonucleotide ligation product is amplified.

"Ligase detection reaction (LDR)" refers to the use of two adjacent oligonucleotides for the detection of specific sequences with the aid of a thermophilic ligase with linear product amplification.

"Ligase DNA sequence" refers to the DNA sequence in *Thermus aqauticus* HB**8** for the thermophilic ligase of the present invention which comprises, at the amino terminus of the ligase protein, the following nucleic acid sequence (SEQ. ID. No. 1):

```
TCCGAATAGG GGATGCGCCC CTAGTCCAAG GGAAAGTATA GCCCACCTA          50

CACTAGGGCC                                                     60

ATG ACC CTG GAA GAG GCG AGG AAG CGG GTA AAC GAG TTA            99

CGG GAC CTC ATC CGC TAC CAC AAC TAC CGC TAC TAC GTC           138

CTG GCG GAC CCG GAG ATC TCC GAC GCC GAG TAC GAC CGG           177

CTT CTT AGG GAG CTC AAG GAG CTT GAG GAG CGC TTC CCC           216

GAG CTC AAA AGC CCG GAC TCC CCC ACC CTT CAG GTG GGG           255

GCG AGG CCT TTG GAG GCC ACC TTC CGC CCC GTC CGC CAC           294

CCC ACC CGC ATG TAC TCC TTG GAC AAC GCC TTT AAC CTT           333

GAC GAG CTC AAG GCC TTT GAG GAG CGG ATA GAA CGG GCC           372

CTG GGG CGG AAG GGC CCC TTC GCC TAC ACC GTG GAG CAC           411

AAG GTG GAC GGG CTT TCC GTG AAC CTC TAC TAC GAG GAG           450

GGG GTC CTG GTC TAC GGG GCC ACC GCC GGG GAC GGG GAG           489

GTG GGG GAG GAG GTC ACC CAG AAC CTC CTC ACC ATC CCC           528

ACC ATC CCG AGG AGG CTC AAG GGG GTG CCG GAG CGC CTC           567

GAG GTC CGG GGG GAG GTC TAC ATG CCC ATA GAG GCC TTC           606

CTC CGG CTC AAC GAG GAG CTG GAG GAG CGG GGG GAG AGG           645

ATC TTC AAA AAC CCT AGG AAT GCG GCG GCG GGT TCC TTA           684

AGG CAA AAA GAC CCC CGC ATC ACC GCC AAG CGG GGC CTC           723

AGG GCC ACC TTC TAC GCC TTA GGG CTT GGG CTG GAG GAG           762

CTG GAG AGG GAA GGG GTG GCG ACC CAG TTT GCC CTC CTC           801

CAC TGG CTC AAG GAA AAA GGC TTC CCC GTG GAG CAC GGC           840

TAC GCC CGG GCC GTG GGG GCG GAA GGG GTG GAG GCG GTC           879

TAC CAG GAC TGG CIC AAG AAG CGG CGG GCG CTT CCC TTT           918

GAG GCG GAC GGG GTG GTG GTG AAG CTG GAC GAG CTT GCC           957

CTT TGG CGG GAG CTC GGC TAC ACC GCC CGC GCC CCC CGG           996

TTC GCC ATC GCC TAC AAG TTC CCC GCC GAG GAG AAG GAG          1035

ACC CGG CTT TTG GAC GTG GTC TTC CAG GTG GGG CGC ACC          1074

GGG CGG GTG ACC CCC GTG GGG ATC CTC GAG CCC GTC TTC          1113

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GAG AGC TAC ATA GAG GAG TTG GAC ATC CGC ATC GGG GAC          1191

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AGG CCC ATT CGC TGG CCC GAG ACC TGC CCC GAG TGC GGC          1308

CAC CGC CTC CTC AAG GAG GGG AAG GTC CAC CGC TGC CCC          1347

AAC CCC TTG TGC CCC GCC AAG CGC TTT GAG GCC ATC CGC          1386

CAC TTC GCC TCC CGC AAG GCC ATG GAC ATC CAG GGC CTG          1425

GGG GAA AAG CTC ATT GAG AGG CTT TTG GAA AAG GGG CTG          1464

GTC AAG GAC GTG GCC GAC CTC TAC CGC TTG AGA AAG GAA          1503

GAC CTG GTG GGC CTG GAG CGC ATG GGG GAG AAG AGC GCC          1542
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CAA AAC CTC CTC CGC GAG ATA GAG GAG AGC AAG AAA AGA          1581

GGC CTG GAG CGC CTC CTC TAC GCC TTG GGG CTT CCC GGG          1620

GTG GGG GAG GTC TTG GCC CGG AAC CTG GCG GCC CGC TTC          1659

GGG AAC ATG GAC CGC CTC CTC GAG GCC AGC CTG GAG GAG          1698

CTC CTG GAG GTG GAG GAG GTG GGG GAG CTC ACG GCG AGG          1737

GCC ATC CTG GAG ACC TTG AAG GAC CCC GCC TTC CGC GAC          1776

CTG GTA CGG AGG CTC AAG GAG GCG GGG GTG GAG ATG GAG          1815

GCC AAG GAG AAG GGC GGG GAG GCC CTT AAA GGG CTC ACC          1854

TCC GTG ATC ACC GGG GAG CTT TCC CGC CCC CGG GAA GAG          1893

GTG AAG GCC CTC CTA AGG CGC CTC GGG GCC AAG GTG ACG          1932

GAC TCC GTG AGC CGG AAG ACG AGC TAC CTC GTG GTG GGG          1971

GAG AAC CCG GGG GAG AAC CCG GGG AGC AAG CTG GAG AAG          2010

GCC AGG GCC CTC GGG GTC CCC ACC CTC ACG GAG GAG GAG          2049

CTC TAC CGG CTC CTG GAG GCG CGG ACG GGG AAG AAG GCG          2088

GAG GAG CTC GTC TAA AGGCTTCC                                 2111
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The corresponding amino acids are (SEQ. ID. No. 2):

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Met Thr Leu Glu Glu Ala Arg Lys Arg Val Asn Glu Leu Arg Asp
                  5                  10                  15

Leu Ile Arg Tyr His Asn Tyr Arg Tyr Tyr Val Leu Ala Asp Pro
                 20                  25                  30

Glu Ile Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys
                 35                  40                  45

Glu Leu Glu Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro
                 50                  55                  60

Thr Leu Gln Val Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro
                 65                  70                  75

Val Arg His Pro Thr Arg Met Tyr Ser Leu Asp Asn Ala Phe Asn
                 80                  85                  90

Leu Asp Glu Leu Lys Ala Phe Glu Glu Arg Ile Glu Arg Ala Leu
                 95                 100                 105

Gly Arg Lys Gly Pro Phe Ala Tyr Thr Val Glu His Lys Val Asp
                110                 115                 120

Gly Leu Ser Val Asn Leu Tyr Tyr Glu Glu Gly Val Leu Val Tyr
                125                 130                 135

Gly Ala Thr Arg Gly Glu Gly Glu Val Gly Glu Glu Val Thr Gln
                140                 145                 150

Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg Arg Leu Lys Gly Val
                155                 160                 165

Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr Met Pro Ile Glu
                170                 175                 180

Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg Gly Glu Arg
                185                 190                 195

Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln
                200                 205                 210

Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr Phe
                215                 220                 225
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-continued

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Tyr Ala Leu Gly Leu Gly Leu Glu Glu Val Glu Arg Glu Gly Val
                230                 235                 240

Ala Thr Gln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Gly Phe
                245                 250                 255

Pro Val Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val
                260                 265                 270

Glu Ala Val Tyr Gln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro
                275                 280                 285

Phe Glu Ala Asp Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu
                290                 295                 300

Try Arg Glu Leu Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile
                305                 310                 315

Ala Tyr Lys Phe Pro Ala Glu Glu Lys Glu Thr Arg Leu Leu Asp
                320                 325                 330

Val Val Phe Gln Val Gly Arg Thr Gly Arg Val Thr Pro Val Gly
                335                 340                 345

Ile Leu Glu Pro Val Phe Leu Glu Gly Ser Glu Val Ser Arg Val
                350                 355                 360

Thr Leu His Asn Glu Ser Tyr Ile Glu Glu Leu Asp Ile Arg Ile
                365                 370                 375

Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val Ile Pro Glu
                380                 385                 390

Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly Glu Glu Arg Pro
                395                 400                 405

Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly His Arg Leu Leu
                410                 415                 420

Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala
                425                 430                 435

Lys Arg Phe Glu Ala Ile Arg His Phe Ala Ser Arg Lys Ala Met
                440                 445                 450

Asp Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu Glu
                455                 460                 465

Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys
                470                 475                 480

Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln
                485                 490                 495

Asn Leu Leu Arg Gln Ile Glu Glu Ser Lys Lys Arg Gly Leu Glu
                500                 505                 510

Arg Leu Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu
                515                 520                 525

Ala Arg Asn Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu
                530                 535                 540

Glu Ala Ser Leu Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu
                545                 550                 555

Leu Thr Ala Arg Ala Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe
                560                 565                 570

Arg Asp Leu Val Arg Arg Leu Lys Glu Ala Gly Val Glu Met Glu
                575                 580                 585

Ala Lys Glu Lys Gly Gly Glu Ala Leu Lys Gly Leu Thr Phe Val
                590                 595                 600

Ile Thr Gly Glu Leu Ser Arg Pro Arg Glu Glu Val Lys Ala Leu
                605                 610                 615

Leu Arg Arg Leu Gly Ala Lys Val Thr Asp Ser Val Ser Arg Lys
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                        -continued
              620                 625                 630

Thr Ser Tyr Leu Val Val Gly Glu Asn Pro Gly Ser Lys Leu Glu
              635                 640                 645

Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr Glu Glu Glu Leu
              650                 655                 660

Tyr Arg Leu Leu Glu Ala Arg Thr Gly Lys Lys Ala Glu Glu Leu
              665                 670                 675

Val
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"Ligating" refers to covalently attaching polynucleotide sequences together to form a single sequence. This is typically performed by treatment with a ligase which catalyzes the formation of a phosphodiester bond between the 5' end of one sequence and the 3' end of the other. However, in the context of the invention, the term "ligating" is also intended to encompass other means of covalently attaching such sequences, e.g., by chemical means. The terms "covalently attaching" and "ligating" may be used interchangeably.

"Nick closing activity" refers to covalent linkage of adjacent strands of DNA. It may be used to assay for ligase activity by virtue of converting open circular DNA (OCDNA) to covalently closed circular DNA (CCCDNA) and determining the speed at which the specimen DNA migrates on an ethidium bromide stained agarose gel (OCDNA migrates slower than CCCDNA).

"Oligonucleotide" refers to a molecule comprised of two or more deoxyribonucleotides or ribonucleotides, preferably more than three. Its exact size will depend on the ultimate function or use of the oligonucleotide. The oligonucleotide may be derived synthetically or by cloning.

"Operably linked" refers to juxtaposition such that the normal function of the components can be performed. Thus, a coding sequence "operably linked" to control sequences refers to a configuration wherein the coding sequences can be expressed under the control of the control sequences.

"Overproducer strain" refers to a strain of bacteria or other host cell that may be induced to overproduce a particular enzyme or chemical substance.

"Polymerase" refers to enzymes which catalyze the assembly of deoxyribonucleotides into DNA.

"Polymerase chain reaction (PCR)" refers to a patented process (described in U.S. Pat. Nos. 4,683,202 and 4,683,195) for the exponential amplification of a specific DNA fragment by utilizing two oligonucleotide primers that hybridize to opposite strands and flank the region of interest in a target DNA. The process consists of a repetitive series of cycles involving template denaturation, primer annealing, and the extension of the annealed primers by Taq DNA polymerase.

"Probe" refers to an oligonucleotide designed to be sufficiently complementary to a sequence in a denatured nucleic acid to be probed (in relation to its length) to be bound under selected stringency conditions. "Contiguous probe" describes a probe which is complementary to the contiguous portion. "Diagnostic probe" describes a probe which is complementary to the diagnostic portion. "Target probe" describes a probe which is complementary to the target sequence and is made by covalently attaching (ligating) the diagnostic probe and the contiguous probe.

"Reporter group" refers to a group that signifies the presence of a particular moiety (see "label").

"Restriction endonucleases" refers to those enzymes which cut DNA by recognizing specific sequences internal to the molecule and subsequently cutting the DNA in both strands at sites either within or outside of the recognition sequence.

"Sticky end ligation" refers to the covalent linkage of two ends of DNA that contain complementary 5' or 3' single strand overhangs which are usually, but not limited to, one to five nucleotides in length.

"Stringency" refers to the combination of conditions to which nucleic acids are subject that cause the double stranded DNA to dissociate into component single strands; among these are pH extremes, high temperature, and salt concentration. "High stringency" refers to the conditions, specifically hybridization and washing, which are sufficient to allow for the detection of unique sequences using an oligonucleotide probe or closely related sequence under standard Southern hybridization protocols [as described in J. Mol. Biol. 98:503-17 (1975)(which discloses hybridization in 2×SSC (i.e. 0.15 M NaCl, 0.015 sodium citrate), 40% formamide at 40° C.)].

"T_m" refers to the temperature at which two complementary strands of DNA unwind and separate. This is a function of the single stranded DNA length and its base composition—for small fragments, an approximate value of T_m in ° C. is equal to 4(G+C)+2(A+T). For example, an oligonucleotide which has 5G, 7C, 5A, and 4T bases has a temperature of 4(5+7)+2(5+4) or 66° C.

"Target sequence" refers to a nucleic acid sequence, the presence or absence of which is desired to be detected. In the context of a preferred application of the method according to the present invention, it is a sequence which forms part of a coding region in a gene associated with a genetic disease, such as sickle-cell anemia. In many such diseases, the presence of the genetic aberration is characterized by small changes in the coding sequence; most frequently, normal individuals have sequences which differ by one nucleotide from the corresponding sequences present in individuals with the genetic "deficiency." In the method according to the present invention, either the normal or altered sequence can be used as the target sequence.

"Thermophilic enzyme" refers to an enzyme which functions at high temperatures of 50 to 90° C.; some may survive brief exposure to temperatures of 94 to 100° C. at which normal enzymes denature and thus become inactive.

"Thermostable ligase" refers to an enzyme which is stable to heat, is heat resistant, and catalyzes (facilitates) ligation, at high temperatures of 50 to 90° C., of adjacent oligonucleotides in the proper manner to form a product which is complementary to the target nucleic acid strand. Generally, the enzyme activates the 5' end of one oligonucleotide and links this to the 3' strand of an adjacent DNA molecules. There may, however, be thermostable enzymes which use other mechanisms to covalently attach adjacent oligonucleotides. Thermostable ligase can, under the proper conditions, covalently link a number of different nucleic acid substrates at high temperatures of 50 to 90° C., such as closing "nicks" in DNA, and sticky end and blunt end ligations.

The thermostable enzyme according to the present invention must satisfy a single criterion to be effective for the amplification reaction, i.e., the enzyme must not become irreversibly denatured (inactivated) when subjected to the elevated temperatures for the time necessary to effect denaturation of double-stranded nucleic acids. By "irreversible denaturation" as used in this connection, is meant a process bringing about a permanent and complete loss of enzymatic activity. The heating conditions necessary for denaturation will depend, e.g., on the buffer salt concentration and the length and nucleotide composition of the nucleic acids being denatured, but typically range from about 85° C., for shorter oligonucleotides, to about 105° C. for a time depending mainly on the temperature and the nucleic acid length, typically from about 0.25 minutes for shorter oligonucleotides, to 4.0 minutes for longer pieces of DNA. Higher temperatures may be tolerated as the buffer salt concentration and/or GC composition of the nucleic acid is increased. Preferably, the enzyme will not become irreversibly denatured at about 90 to 100° C. The thermostable enzyme according to the present invention has an optimum temperature at which it functions that is greater than about 45° C., probably between 50 and 90° C., and optimally between 60 and 80° C.

A more thorough and complete understanding of the cloning of the thermophilic ligase sequence and the use of this enzyme in the thermophilic ligase mediated DNA amplification procedure for the detection of single base pair sequence differences in genetic diseases can be obtained by reference to the following figures and examples which are presented by way of illustration only and are not intended, nor should they be considered, to limit the scope of the claimed invention.

With specific reference to the figures,

FIG. **1** is a depiction of plasmids pDZ**1** and pDZ**7**;

FIG. **2** is a flow chart of the Ligase Chain Reaction (LCR) according to the present invention;

FIG. **3** is an autoradiogram demonstrating the specificity of *T. aquaticus* thermophilic ligase under both LDR and LCR amplification conditions according to the present invention;

FIG. **4** is an autoradiogram demonstrating LCR amplification at different target concentrations;

FIG. **5** is an autoradiogram demonstrating the detection of β globin alleles using human genomic DNA.

FIG. **6** is an overview of an ELISA based oligonucleotide ligation assay according to the present invention.

FIG. **7** is a photographic representation of SDS-10% polyacrylamide gel electrophoresis of the thermostable ligase, according to the present invention, at different stages of purification.

FIG. **8** is a second photographic representation of SDS-10% polyacrylamide gel electrophoresis of the thermostable ligase, according to the present invention, at different stages of purification.

FIG. **9** is a depiction of three clones prepared in accordance with the present invention.

In FIG. **7**, lanes A and G represent marker proteins (molecular weights are given in kd); B represents whole cells after induction; C represents crude supernatant after sonication;

D represents pooled DEAE flow-through after heat treatment; and E and F represent fractions **23** and **24** after phosphocellulose chromatography. In FIG. **8**, lanes A and H represent marker proteins (molecular weights are given in kd); B represents whole cells after induction; C represents crude supernatant after sonication; D represents pooled DEAE flow-through after heat treatment; E represents fraction **23** after phosphocellulose chromatography; F represent fraction **23** incubated with nicked DNA in ligase buffer in the absence of NAD; and G represents fraction **23** incubated with NAD in ligase buffer in the absence of nicked DNA. In FIG. **8**, the higher molecular weight ligase (approximately 81 kd) is the adenylated form, while lower molecular weight ligase (approximately 78 kd) is non-adenylated.

The plasmids depicted in FIG. **1** have been deposited with, and accepted by, a collection agency under the Budapest Treaty deposit rules. Plasmid pDZ**1** has been incorporated within a host bacteria (*E. coli* strain AK**53**), deposited with the American Type Culture Collection, and granted the collection number ATCC No. 68307. Plasmid pDZ**7** has been incorporated within a host bacteria (*E. coli* strain AK**53**), deposited with the American Type Culture Collection, and granted the collection number ATCC No. 68308.

While other methods may be used, in general, the production of the thermophilic ligase according to the present invention will be by recombinant means which typically involve the following:

First, a DNA is obtained which encodes the mature (as used herein the term includes all muteins) enzyme or a fusion of the thermophilic ligase to an additional sequence that does not destroy its activity or to an additional sequence cleavable under controlled conditions to give an active protein. If the sequence is uninterrupted by introns, it is suitable for expression in any host. However, the sequence should be in an excisable and recoverable form. Using PCR technology, for example, most DNA sequences coding for enzymes may be amplified and hence recovered in an "excised" form.

The excised or recovered coding sequence is then placed in operable linkage with suitable control sequences in a replicable expression vector which is used to transform a suitable host. The transformed host is then cultured under suitable conditions to effect the production of the recombinant thermophilic ligase, and the ligase isolated and purified by known means.

Each of the above procedures may be accomplished in a variety of ways, For example, the desired coding sequences may be obtained from genomic fragments and used directly in appropriate hosts; the constructions for expression vectors operable in a variety of hosts are made using appropriate replicons and control sequences; and suitable restriction sites may, if not normally available, be added to the ends of the coding sequence so as to provide an excisable gene to insert into the appropriate vector.

The control sequences, expression vectors, and transformation methods are dependent on the type of host cell used to express the gene. Generally, bacterial hosts are the most efficient and convenient for the production of recombinant proteins and therefore preferred for the expression of the thermophilic ligase according to the present invention. However, other hosts such as yeast, plant, and insect or mammalian cells may also be used if convenient. For the purposes of the present invention, one source of the host cell is considered to be equivalent to any other available and suitable host cell source.

EXAMPLE I

Growth of *T. aquaticus* Strain HB**8** and Isolation of DNA

DNA was isolated from *Thermus thermophilus* strain HB**8** (ATCC No. 27634). This strain has recently been reclassified as *Thermus aquaticus* strain HB**8** [see Arch. Microbiol 117:189 (1978)].

Cells were grown overnight at 75° C. in a water bath shaker in TAB broth [see Nuc. Acids Res., pgs 6795–6804 (1981)] (which contains per liter, 5 g Bacto™-tryptone, 3 g yeast extract, 2 g NaCl, and 1 g dextrose) adjusted to pH 7.2–7.5 with NaOH, and harvested by centrifugation to yield 3.1 g wet weight from 800 ml of media. Cells were resuspended in 15 ml of 50 mM Tris pH 8.0 buffer containing 50 mM EDTA and 15 mg egg white lysozyme. The resuspended cells were lysed by the addition of 2 ml of 10% (weight/volume) sodium dodecyl sulfate followed by incubation at 37° C. for 15 minutes and two repeated cycles of freezing at −50° C. and thawing at 37° C. The aqueous solution was extracted sequentially with equal volumes of aqueous phenol (preequilibrated to pH 7.5 with sodium borate), followed by phenol/chloroform, and finally chloroform.

Nucleic acids were precipitated by mixing with 2 volumes of 95% ethanol, chilling to −50° C. for 15 min., and pelleted by centrifugation. After removal of the supernatant and drying the pellet, nucleic acids were resuspended in 1 ml TE buffer (10 mM Tris HCl, pH 8.0, containing 1 mM EDTA). RNA was digested by the addition of 100 μg RNase A to each ml of suspension, and the mixture incubated at 37° C. for 1 hr. DNA was precipitated by adding 1/10th vol. of 3 M sodium acetate and 3 vol. of 100% ethanol, chilled to −50° C. for 15 min., pelleted by centrifugation, washed with 70% ethanol, and finally resuspended in TE buffer at a final concentration of 2 mg/ml.

Although DNA utilized in the example given above was isolated from *Thermus aquaticus,* the resultant thermophilic ligase having the necessary properties according to the present invention may have as its initial source DNA isolated from other *Thermus* species or other thermophilic bacteria, phages, or viruses.

DNA isolated from *T. aquaticus* strain HB**8** cannot be cleaved by the restriction endonucleases Taq I (whose recognition sequence is TCGA) or EcoRI (whose recognition sequence is GAATTC). The inability to cleave certain sequences is a consequence of protective methylation [see H. O. Smith and S. V. Kelly, DNA Methylation: Biochemistry and Biological Significance, eds. Razin, Cedar and Riggs, p 39–71, Springer-Verlag Inc., New York (1987)] at the N**6** position of adenine residues. Previous investigators [see J. Bact. 169:3243 (1987)] have shown that there is a gene, termed mrr, which restricts adenine methylated DNA of the form G-6MeANTC and CTGC-6MeAG. In the cloning of the Taq I restriction endonuclease and methylase, several *E. coli* strains were found to restrict the TCGA methylated DNA, an affect originally (but incorrectly) attributed to the mrr gene [see Gene 56:13 (1987) and Nuc. Acid Res. 15:9781 (1987)]. Recent work conducted at the Cornell University Medical College has shown the presence of an additional gene, besides mrr which encodes a protein that restricts TCGA methylated DNA. Briefly, strains containing a Tn**5** (Km^R) transposon disrupting the mrr gene were [see J. Bact. 169:3243 (1987)] used for transduction [according to J. H. Miller in Experiments in Molecular Genetics, Cold Spring Harbor Laboratory, pp 201–205 (1972)] of the Km^R marker into several strains of *Escherichia coli* that resulted in strain converts to a mrr—(defective mrr protein) genotype. None of these transduced strains could tolerate the Taq methylase gene, indicating there is a second gene responsible for the restriction of TCGA methylated DNA. Thus, one of the first necessary requirements (which prior to the present invention had not been apparent) for the making of the present invention was the selection of an *E. coli* strain which would not heavily restrict TCGA methylated DNA.

In the present invention, a derivative of the RRI strain of *E. coli* which could tolerate the Taq methylase gene and which contained a Tn**10** (Tc^R) transposon was transduced to a ligts**7** strain [N3098, see Wilson and Murray, J. Mol. Biol. (1979) and J. Mol. Biol. 77:531 (1973)] to create *E. coli* strain AK**76**. This strain has been deposited in the American Type Culture Collection, and has been granted the collection number ATCC No. 55032. This strain contains a temperature sensitive ligase gene, such that at 42° C. the strain cannot grow. This strain can tolerate the Taq methylase gene, and other methylated DNA, especially the DNA isolated from *T. aquaticus.* Since it also has a temperature sensitive ligase gene, it could be used as a host for the cloning of a functional *T. aquaticus* ligase gene by selecting for growth at 42° C.

Cloning of the *T. aquaticus* ligase gene was based on a positive selection scheme similar to that described by Wilson and Murray. The approach was to construct libraries of *T. aquaticus* DNA inserted into a suitable vector. These libraries were then introduced via transformation into a ligts**7** *E. coli* strain that did not restrict methylated *T. aquaticus* DNA, such as strain AK**76**. These cells were then grown at the nonpermissive temperature, that is at 42° C. Any survivors could be (i) revertants to a lig+phenotype; (ii) second site revertants that increase expression of the defective *E. coli* ligase gene product; (iii) a cloned piece of *T. aquaticus* DNA that increases expression of the defective *E. coli* ligase gene product; or (iv) a cloned piece of *T. aquaticus* DNA that contains the *T. aquaticus* ligase gene.

For the desired last alternative to work, it is necessary that (i) the entire ligase gene is cloned; (ii) that either the endogenous control sequences for *T. aquaticus* ligase expression function in *E. coli,* or that exogenous vector control sequences are sufficiently close to the amino terminus and the ligase gene is cloned in the correct orientation to allow for proper expression in *E. coli;* (iii) the *T. aquaticus* ribosome binding site works in *E. coli;* and (iv) the *T. aquaticus* ligase is active enough at 42° C., and the amount synthesized is sufficient to complement ligase function in *E. coli* without interfering with other processes.

Construction of the suitable libraries used in the present invention utilized conventional vectors containing desired control sequences, and standard restriction endonuclease and ligation techniques. Purified plasmid DNA, *T. aquaticus* DNA sequences, or synthesized oligonucleotides for use in the present invention, were cleaved, tailored, and religated in the form desired also by conventional techniques.

The selection of a suitable vector for use in the present invention is more than a mere matter of selecting a vector among the many which exist and have been used in the past. High copy number derivatives of pUC plasmids [see for example, C. Yanisch-Peron et al., Gene 33:103 (1985), or J. Vieira et al., Gene 19:259 (1982)] are actually somewhat unstable when grown at 42° C. Low copy plasmids such as pBR**322** derivatives pFBI **1, 2, 13, 14** and **15** [see F. Barany, Proc. Natl. Acad. Sci. USA 82:4202 (1985)] may not produce enough enzyme to complement the ligase defect. In making the present invention, 18 different libraries using 3 different sets of vectors were constructed. The successful clone was derived from the vector pTZ18R [see D. A. Mead et al., Protein Engineering 1:67 (1986)], although other vectors may also be utilizable.

Generally, site-specific DNA cleavage, as more particularly described in the following example, is performed by treating the DNA with a suitable restriction enzyme under conditions which are generally understood in the art, and the particulars of which are specified by the manufacturers of these commercially available restrictions enzymes. In general, about 1 μg of plasmid or DNA sequence is cleaved by two to ten units of enzyme in about 20 μl of buffer solution. Incubation times of about one to two hours at about 37° C. are preferable, although variations in both the time and temperature can be tolerated. After each incubation, protein is removed by extraction with phenol/chloroform, and may be followed by a further extraction. The nucleic acids are recovered by precipitation with ethanol. If desired, size separations of the cleaved fragments may be performed by polyacrylamide or agarose gel electrophoresis using standard techniques.

EXAMPLE II

Site Specific Cleavage

Site-specific cleavage of both plasmid and *T. aquaticus* DNA was performed using commercially available restriction endonucleases in standard buffers.

In general, about 10 μg or plasmid or *T. aquaticus* DNA was cleaved in 100 μl of buffer solution by the addition of 20 to 100 units of the appropriate restriction endonuclease, and incubating the mixture at 37° C. for 1 to 2 hrs.

After each incubation, protein was removed by sequential extractions with phenol (2x), n-butanol (2x), and the nucleic acid was recovered by precipitation with ethanol.

Construction of suitable vectors containing the desired coding and control sequences employs conventional ligation and restriction techniques. Briefly, isolated plasmids, DNA sequences, or synthesized oligonucleotides are cleaved, tailored, and religated in the form desired.

The restriction endonucleases utilized for cleavage of the specific libraries used in accordance with the procedure outlined in Example II were BamHI, SacI, KpnI (Asp**718**), PstI, HindIII, and SmaI, however, other endonucleases or partial digests with SauIIIA, for example, could have been used. Due to adenosine methylation, the commonly utilized restriction endonucleases EcoRI, SalI or XhoI were not used since DNA from *T. aquaticus* strain HB**8** could not be cleaved by these enzymes.

Restriction fragments resulting from the procedure outlined in Example II containing 5' overhangs may be blunt ended by filling in with DNA polymerase I large (Klenow fragment) in the presence of the four deoxynucleotide triphosphates using incubation times of about 15 to 30 minutes at 37° C. in 50 mM Tris pH 7.6 buffer containing 50 mM NaCl, 10 mM $MgCl_2$, 10 mM DTT, and 50–100 μM deoxynucleotide triphosphates. The Kienow fragment will fill in at 5' sticky ends. If 3' overhangs are generated, they may be chewed back with mung bean nuclease. After treatment with Klenow, the mixture is extracted with phenol/chloroform and precipitated with ethanol. Subsequent treatment under appropriate conditions with S**1** nuclease results in hydrolysis of any single stranded portion. These conventional procedures may be used for cloning any fragment into a (blunt end) site within the vector.

EXAMPLE III

Vector Construction

In vector constructions, the linearized vector is commonly treated with a phosphatase enzyme (or alternatively with a second nearby restriction endonuclease) to prevent recircularization of the vector in the absence of insert DNA. For example, a sample of BamHI (5' overhang) or SacI (3' overhang) DNA (9 μg) in 150 μl 50 mM Tris HCl buffer at pH 8.0 and containing 10 mM $MgCl_2$ and 6 mM mercaptoethanol in the presence of Na+ may be treated with Calf Intestine Alkaline Phosphatase (CIAP, 22 units) at 37° C. for 15 min., followed by incubation at 50° C. for 30 min. to remove phosphate groups from either 5' or 3' overhangs. Alternatively, Bacterial Alkaline Phosphatase (BAP, 10 units) may be used in 150 μl 10 ml Tris HCl in the presence of Na+ and Mg++ and incubating at 60° C. for about 1 hr. CIAP may be subsequently denatured by the addition of EDTA and EGTA to chelate divalent cations, and heating to 65° C. for 15 min. Either CIAP or BAP protein is them removed by sequential extractions with phenol (2x), n-butanol (2x), and nucleic acid recovered by precipitation with ethanol.

The effectiveness of the phosphatase step is assayed by comparison of the number of transformants generated when vector is religated in the absence or presence of insert DNA. Typical results of from 10 to 100 fold more transformations when insert DNA is present is indicative that the vector DNA has been properly phosphatased.

EXAMPLE IV

Ligations

Ligations were performed in 30–100 μl volumes using 1–2 μg linearized and phosphatased vector made as previously described. 2–4 μg *T. aquaticus* DNA cut with a restriction endonuclease generating the same ends as the vector, in 50 mM Tris HCl buffer at pH 8.0 and containing 10 mM $MgCl_2$, 1 mM EDTA, 1 mM ATP, 6 mM mercaptoethanol and from 3 to 7 (Weiss) units of T**4** ligase, by incubating at either 4 or 15° C. overnight. After ligation, EDTA was added, the T**4** ligase inactivated by heating the solution to 65° C. for 15 min., and nucleic acids recovered by ethanol precipitation.

Ligation mixtures were introduced into a suitable host such as *E. coli* strains RR**1**, AK**53** or AK**76**—the last one suitable for immediate positive selection of the lig+ phenotype—via conventional transformation procedures [see Hanahan, J. Mol. Biol. 166:3243 (1987)]. Transformants were selected by plating on ampicillin (or other drugs such as tetracycline or kanamycin depending upon the plasmid used) containing plates. For positive selection of the lig+ phenotype, AK**76** transformants were plated onto SOB plates (made by autoclaving 20 g Bacto™-tryptone, 5 g Bacto™-yeast extract, 0.5 g NaCl, 16 g Bacto™-agar in 1 liter of distilled water adjusted to pH 7.5 with NaOH prior to autoclaving, then adding 20 ml 1 M $MgSO_4$) containing 0.2% maltose, 0.2 mg/ml IPTG (to induce the lac promoter), and 50 μg/ml ampicillin (to select the plasmid-containing cells), and grown overnight at 42° C. to 42.5° C.

Libraries ranged in size from about 5,000 to 27,000 clones. Given the general estimate that the bacterial chromosome contains about 2,000 to 4,000 kilobases, and the average insert consisted of 5 to 10 kb, it was apparent that several libraries contained redundant clones.

Mixed plasmid preparations were made from six libraries using conventional techniques [see Methods Enzymol. 100:243 (1983)], and introduced into fresh AK**76** cells. Transformants from each library were plated on 6 SOB plates (each plate receiving between 30,000 and 70,000 clones) and incubated at 42° C. One library produced from 11 to 19 exceedingly small colonies per plate; the remaining libraries produced an occasional large colony.

Individual clones were picked, plasmid DNA prepared using conventional techniques [see Anal. Biochem. 114:193 (1981)], and analyzed by restriction digestion. All 12 small clones produced a 6.8 kb plasmid containing two BamHI fragments (1.8 and 2.1 kb respectively) cloned within the BamHI site of pTZ**18**R. One such plasmid has been designated pDZ**1** as depicted in FIG. **1**. By calculating back to the original library, (of 5,200 clones), it appears that all pDZ**1** plasmids derived from a single clone. The large colonies contained plasmids close to the size of the original vector. Therefore, these large colonies are probably revertants of the chromosomal ligts**7** gene which contained any plasmid solely to confer resistance to ampicillin.

Retransforming plasmid pDZ**1** into AK**76** cells, and selecting at 42° C. on SOB plates containing maltose, IPTG, and ampicillin as described in Example IV, again yielded small colonies. Plating fresh transformants on tryptone yeast agar containing ampicillin did not produce colonies. This result suggests that induction of the lac promoter during plasmid establishment is necessary for production of sufficient quantities of *T. aquaticus* ligase to complement the genetic defect. Once the plasmid has become established in AK**76** cells, such clones will give exceedingly small colonies when streaked and allowed to grow on tryptone yeast plates containing ampicillin at 42° C.

Digestion of pDZ**1** with BamHI, followed by religation would scramble the fragments. Transformation of such a ligation mix into AK**76**, followed by plating at 37° C., i.e. under non-selective conditions, compared to plating at 42° C., i.e. under selective conditions, yielded 1,000 fold more colonies under non-selective conditions. The starting pDZ**1** plasmid yielded only 2 fold more colonies under non-selective than selective conditions. This finding strongly suggests that the presence of both fragments, and the orientation they are cloned, is necessary for proper expression of *T. aquaticus* ligase.

Although pDZ**1** contains several SacI and SmaI sites, it only contains a single (vector derived) PstI, KpnI, or HindIII site. Thus, it would have been expected that a number of ligase clones would have been isolated from the PstI, KpnI, or HindIII digest libraries. However, the only ligase clone was derived from the partial BamHI digest library. Although it is not clear why this happened, one conceivable explanation is that other clones did not bring the lac promoter controlling element sufficiently close to the start of the ligase gene to adequately express the ligase protein during plasmid establishment.

The cloning of *T. aquaticus* ligase as described above will now enable those skilled in the art to clone any thermophilic or thermostable ligase, whether of procaryotic, archebacterial, eukaryotic or phage origin by additional approaches. Accordingly the cloning of such ligases are within the scope of the present invention.

Such additional approaches to cloning may include, for example, (i) cloning *T. aquaticus* DNA into a red-lambda vector and screening for the ability of recombinant phage lambda to form plaques at 39° C. on a ligts**7** strain such a AK**76** [essentially as generally described in J. Mol. Biol. 132:471 (1979)]; (ii) use of the lambda gt**11** phage to express portions of the ligase gene, and subsequently screening with antibodies raised to purified *T. aquaticus* ligase—the positive lambda gt**11** clone may then be used to identify the full length gene by hybridization to other plasmid or phage libraries, essentially as described in the cloning of *T. aquaticus* polymerase [see J. Biol. Chem 264:6427 (1989)]; 90(iii) based upon the ligase DNA sequence, probes can be made that would hybridize to and therefore help to identify and retrieve other thermostable ligase encoding sequences in a variety of species. Accordingly, portions of the DNA encoding at least five amino acids from *T. aquaticus* ligase can be replicated, or amplified using PCR techniques, and the denatured or single stranded forms may be used as probes to retrieve additional DNAs encoding a thermophilic or thermostable ligase. Alternatively, oligodeoxyribonucleotide probes can be synthesized which encode at least five amino acids, and these may be used to retrieve additional DNAs encoding a thermophilic or thermostable ligase.

The selection of a portion of DNA encoding for at least five amino acids is based upon the portion containing fifteen nucleic acid bases which is more than the statistical minimum length that an oligonucleotide should have in order to find a single complementary sequence in a genome. However, portions slightly smaller (the minimum number in *E. coli* is, for example 12, indicating a portion as small as that encoding for four amino acids may be acceptable) or larger (the minimum number for higher animals is as high as 19, indicating that a portion encoding for at least seven amino acids may be necessary) [see Oligonucleotides: Antisense Inhibitors of Gene Expression, vol. 12, pages 137–140, Macmillan Press Ltd., London (1989)] may be used to obtain similar results However, because there may not be a precise match between the nucleotide sequence in the corresponding portions between species, oligomers containing approximately 15 nucleotides are a preferred minimum in order to achieve hybridization under conditions of sufficient stringency to eliminate false positives; the sequence encoding 5 amino acids would supply information sufficient for the generation of such probes.

By way of example, a comparison of the *T. aquaticus* ligase and *E. coli* amino acid sequences reveals an identity between amino acids 34–40 (Asp-Ala-Glu-Tyr-Asp-Arg-Leu)(SEQ. ID. No. 3) at statistically acceptable levels. Using the preferred six amino acid sequence, a degenerate probe of the form GA(C/T)-GC(G/A/T/C)-GA(G/A)-TA(C/T)-GA(C/T)-(C/A)G(G/A/T/C)-(C/T)T (SEQ. ID. No. 4) could be used to identify and retrieve either of the above ligases. The areas of sequence identities between the *Thermophilus* ligase according to the present invention and *E. coli* ligase include the amino acids at the following positions:

Amino Acid Positions	Consecutive identical aa's
34 to 40	7
57 to 61	5
137 to 142	6
168 to 175	8
199 to 210	12
212 to 219	8
308 to 312	5
333 to 339	7
485 to 490	6
492 to 496	5
513 to 517	5
620 to 624	5

Overall, of the 676 amino acids contained in the ligase according to the present invention, the percent similarity between the *Thermophilus* ligase and *E. coli* ligase is 66%; the percent identity is 47%.

The construction of an overproducer strain from a cloned and properly oriented gene may be achieved by using procedures which are conventional in the art. The general principle of such construction is to bring an enabling sequence into close proximity to the starting codon of the gene to affect efficient transcription and translation of that gene. There are many promoter systems (including a ribosome binding site [see Proc. Natl. Acad. Sci. USA 78:5543 (1981)]) that have been successfully used to turn on genes, including the lac promoter, the trp promoter [see Gene 20:231 (1982)], the lambda phage P_L promoter [see Nature 292:128 (1981)], the tac fusion promoter [see Proc. Natl. Acad. Sci. USA 80:21 (1983)], and the T7 phage promoters [see Proc. Natl. Acad. Sci. USA 82:1074 (1985)].

Plasmid pDZ1 contains the *T. aquaticus* ligase gene downstream from both lac and T7 promoters present in the starting vector. There are several methods for removing excess DNA sequences from between the promoters and the gene, including use of Bal**31** [see Nucl. Acids Res. 5:1445 (1978)] and ExoIII and Mung Bean or S_1 Nuclease [see Meth. Enzymol. 155:156 (1987)]. However, a somewhat simpler method as described in Example V was used to bring the amino terminus of the *T. aquaticus* ligase gene closer to the two promoters in the present instance.

EXAMPLE V

Removal of Excess DNA From Between Promoter and Gene

Plasmid pDZ1 was randomly linearized with the restriction endonuclease HinPI (G CGC) and blunt ended with Klenow or alternatively with CviJI (PuG CPy) [see DNA and Protein Engineering Techniques 1:29 (1988)].

DNA was purified by sequential extractions with phenol (2 x), n-butanol (2 x), and the nucleic acid recovered by precipitation with ethanol. These randomly linearized plasmids were then treated with Asp**718** which cleaves the polylinker site directly downstream of the two promoters, and blunt ended with Klenow. The resulting fragments were separated via electrophoresis in low melting agarose, sequential slices (including full length linear and progressively smaller DNA fragments) excised, and the DNA recovered. The DNA fragments were subsequently recircularized by blunt end ligation. This involved overnight incubation at 4° C. in 100 μl in 50 mM Tris HCl pH 8.0 buffer containing 10 mM $MgCl_2$, 1 mM EDTA, 1 mM ATP, 6 mM mercaptoethanol, and from 3 to 7 Weiss units of T**4** ligase. After ligations, EDTA was added, the T**4** ligase inactivated by heat (for 15 min at 65° C.), and nucleic acids recovered by ethanol precipitation.

The ligation mixes prepared were introduced into AK**76** cells using conventional techniques, and the lig+ phenotype was selected at 42° C. on SOB plates containing maltose, IPTG, and ampicillin as described previously.

Based upon previous work, plasmids containing deletions between the promoters and the start of the *T. aquaticus* ligase gene would be expected to confer viability under these conditions. Deletions of the vector (promoter regions), or of an essential portion of the ligase gene should not confer viability. Therefore, individual clones were picked, plasmid DNA prepared using conventional methods [see Anal. Biochem. 114:193 (1981)], and analyzed by restriction digestion. Results from this testing found that plasmid pDZ**2**, pDZ**3**, pDZ**6** and pDZ**7** lacked the 1.8 kb BamHI fragment, and contained instead a 1.3, 1.4, 1.2, or 1.2 kb fragment, respectively. All these plasmids re-created the Asp**718** site as would be expected with proper blunt end fill-ins and ligations. Single stranded DNA was prepared from these plasmids using conventional techniques [see Nucl. Acids Research 13:1103 (1985), and Protein Engineering 1:64 (1986)], and these were sequenced using the universal "reverse primer" oligonucleotide 5'd (AGCGGATAACAATTTCACACAGGA)3'(SEQ. ID. No. 5) and T**7** DNA polymerase [see Proc. Natl, Acad. Sci. USA 84:4767 (1987)].

Analysis of the DNA sequence reveals two ATG start codons, the first open reading frame being three codons in length and the second, the ligase DNA sequence, giving a long reading frame. In conjunction with FIG. **1**, this sequence (including the partial ligase DNA sequence) derived from plasmids pDZ**6** and pDZ**7** is:

```
     pTZ18R (SEQ. ID. No. 6)
GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT

                         LacZ'      T7 Promoter
CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTAATA

                                          pDZ6,7
CGACTCACTA TAGGGAATTC GAGCTCGGTA CCCCAAGGTA
               EcoRI  SacI   KpnI

CACTAGGGCC
     thermophilic ligase (SEQ. ID. No. 7)

ATG ACC CTG GAA GAG GCG AGG AAG CGG GTA AAC GAG TTA          39

CGG GAC CTC ATC CGC TAC CAC AAC TAC CGC TAC TAC GTC          78

CTG GCG GAC CCG GAG ATC TCC GAC GCC GAG TAC GAC CGG         117

CTT CTT AGG GAG CTC AAG GAG CTT GAG GAG CGC TTC CCC         156

GAG CTC AAA AGC CCG GAC TCC CCC ACC CTT CAG GTG GGG         195

GCG AGG CCT TTG GAG GCC ACC TTC CGC CCC GTC CGC CAC         234

CCC ACC CGC ATG TAC TCC TTG GAC AAC GCC TTT AAC CTT         273

GAC GAG CTC AAG GCC TTT GAG GAG CGG ATA GAA CGG GCC         312
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-continued

CTG GGG CGG AAG GGC CCC TTC GCC TAC ACC GTG GAG CAC 351

AAG GTG GAC GGG CTT TCC GTG AAC CTC TAC TAC GAG GAG 390

GGG GTC CTG GTC TAC GGG GCC ACC GCC GGG GAC GGG GAG 329

GTG GGG GAG GAG GTC ACC CAG AAC CTC CTC ACC ATC CCC 368

ACC ATC CCG AGG AGG CTC AAG GGG GTG CCG GAG CGC CTC 407

GAG GTC CGG GGG GAG GTC TAC ATG CCC ATA GAG GCC TTC 446

CTC CGG CTC AAC GAG GAG CTG GAG GAG CGG GGG GAG AGG 483

ATC TTC AAA AAC CCT AGG AAT GCG GCG GCG GGT TCC TTA 524

AGG CAA AAA GAC CCC CGC ATC ACC GCC AAG CGG GGC CTC 563

AGG GCC ACC TTC TAC GCC TTA GGG CTT GGG CTG GAG GAG 602

GTG GAG AGG GAA GGG GTG GCG ACC CAG TTT GCC CTC CTC 641

CAC TGG CTC AAG GAA AAA GGC TTC CCC GTG GAG CAC GGC 680

TAC GCC CGG GCC GTG GGG GCG GAA GGG GTG GAG GCG GTC 719

TAC CAG GAC TGG CTC AAG AAG CGG CGG GCG CTT CCC TTT 758

GAG GCG GAC GGG GTG GTG GTG AAG CTG GAC GAG CTT GCC 797

CTT TGG CGG GAG CTC GGC TAC ACC GCC CGC GCC CCC CGG 836

TTC GCC ATC GCC TAC AAG TTC CCC GCC GAG GAG AAG GAG 875

ACC CGG CTT TTG GAC GTG GTC TTC CAG GTG GGG CGC ACC 914

GGG CGG GTG ACC CCC GTG GGG ATC CTC GAG CCC GTC TTC 953

CTA GAG GGC AGC GAG GTC TCC CGG GTG ACC CAC CAC AAC 992

GAG AGC TAC ATA GAG GAG TTG GAC ATC CGC ATC GGG GAC 1031

TGG GTT TTG GTG CAC AAG GCG GGC GGG GTC ATC CCC GAG 1070

GTC CTC CGG GTC CTC AAG GAG AGG CGC ACG GGG GAG GAA 1109

AGG CCC ATT CGC TGG CCC GAG ACC TGC CCC GAG TGC GGC 1148

CAC CGC CTC CTC AAG GAG GGG AAG GTC CAC CGC TGC CCC 1187

AAC CCC TTG TGC CCC GCC AAG CGC TTT GAG GCC ATC CGC 1226

CAC TTC GCC TCC CGC AAG GCC ATG GAC ATC CAG GGC CTG 1265

GGG GAA AAG CTC ATT GAG AGG CTT TTG GAA AAG GGG CTG 1304

GTC AAG GAC GTG GCC GAC CTC TAC CGC TTG AGA AAG GAA 1343

GAC CTG GTG GGC CTG GAG CGC ATG GGG GAG AAG AGC GCC 1382

CAA AAC CTC CTC CGC GAG ATA GAG GAG AGC AAG AAA AGA 1421

GGC CTG GAG CGC CTC CTC TAC GCC TTG GGG CTT CCC GGG 1460

GTG GGG GAG GTC TTG GCC CGG AAC CTG GCG GCC CGC TTC 1499

GGG AAC ATG GAC CGC CTC CTC GAG GCC AGC CTG GAG GAG 1538

CTC CTG GAG GTG GAG GAG GTG GGG GAG CTC ACG GCG AGG 1577

GCC ATC CTG GAG ACC TTG AAG GAC CCC GCC TTC CGC GAC 1616

CTG GTA CGG AGG CTC AAG GAG GCG GGG GTG GAG ATG GAG 1655

GCC AAG GAG AAG GGC GGG GAG GCC CTT AAA GGG CTC ACC 1694

TCC GTG ATC ACC GGG GAG CTT TCC CGC CCC CGG GAA GAG 1733

GTG AAG GCC CTC CTA AGG CGC CTC GGG GCC AAG GTG ACG 1772

-continued

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GAC TCC GTG AGC CGG AAG ACG AGC TAC CTC GTG GTG GGG       1811

GAG AAC CCG GGG GAG AAC CCG GGG AGC AAG CTG GAG AAG       1850

GCC AGG GCC CTC GGG GTC CCC ACC CTC ACG GAG GAG GAG       1889

CTC TAC CGG CTC CTG GAG GCG CGG ACG GGG AAG AAG GCG       1928

GAG GAG CTC GTC TAA AGGCTTCC                              1971
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The nucleic acid sequence for the thermophilic ligase according to the present invention corresponds to the amino acid sequence (SEQ. ID. No. 8):

```
Met Thr Leu Glu Glu Ala Arg Lys Arg Val Asn Glu Leu Arg Asp
                  5                  10                  15

Leu Ile Arg Tyr His Asn Tyr Arg Tyr Tyr Val Leu Ala Asp Pro
                 20                  25                  30

Glu Ile Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys
                 35                  40                  45

Glu Leu Glu Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro
                 50                  55                  60

Thr Leu Gln Val Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro
                 65                  70                  75

Val Arg His Pro Thr Arg Met Tyr Ser Leu Asp Asn Ala Phe Asn
                 80                  85                  90

Leu Asp Glu Leu Lys Ala Phe Glu Glu Arg Ile Glu Arg Ala Leu
                 95                 100                 105

Gly Arg Lys Gly Pro Phe Ala Tyr Thr Val Glu His Lys Val Asp
                110                 115                 120

Gly Leu Ser Val Asn Leu Tyr Tyr Glu Glu Gly Val Leu Val Tyr
                125                 130                 135

Gly Ala Thr Arg Gly Glu Gly Glu Val Gly Glu Glu Val Thr Gln
                140                 145                 150

Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg Arg Leu Lys Gly Val
                155                 160                 165

Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr Met Pro Ile Glu
                170                 175                 180

Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg Gly Glu Arg
                185                 190                 195

Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln
                200                 205                 210

Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr Phe
                215                 220                 225

Tyr Ala Leu Gly Leu Gly Leu Glu Glu Val Glu Arg Glu Gly Val
                230                 235                 240

Ala Thr Gln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Gly Phe
                245                 250                 255

Pro Val Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val
                260                 265                 270

Glu Ala Val Tyr Gln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro
                275                 280                 285

Phe Glu Ala Asp Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu
                290                 295                 300

Try Arg Glu Leu Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile
                305                 310                 315
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                         -continued

Ala Tyr Lys Phe Pro Ala Glu Glu Lys Glu Thr Arg Leu Leu Asp
                320                 325                 330

Val Val Phe Gln Val Gly Arg Thr Gly Arg Val Thr Pro Val Gly
                335                 340                 345

Ile Leu Glu Pro Val Phe Leu Glu Gly Ser Glu Val Ser Arg Val
                350                 355                 360

Thr Leu His Asn Glu Ser Tyr Ile Glu Glu Leu Asp Ile Arg Ile
                365                 370                 375

Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val Ile Pro Glu
                380                 385                 390

Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly Glu Glu Arg Pro
                395                 400                 405

Ile Arg Trp Pro Glu Thr Gys Pro Glu Cys Gly His Arg Leu Leu
                410                 415                 420

Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala
                425                 430                 435

Lys Arg Phe Glu Ala Ile Arg His Phe Ala Ser Arg Lys Ala Met
                440                 445                 450

Asp Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu Glu
                455                 460                 465

Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys
                470                 475                 480

Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln
                485                 490                 495

Asn Leu Leu Arg Gln Ile Glu Glu Ser Lys Lys Arg Gly Leu Glu
                500                 505                 510

Arg Leu Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu
                515                 520                 525

Ala Arg Asn Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu
                530                 535                 540

Glu Ala Ser Leu Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu
                545                 550                 555

Leu Thr Ala Arg Ala Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe
                560                 565                 570

Arg Asp Leu Val Arg Arg Leu Lys Glu Ala Gly Val Glu Met Glu
                575                 580                 585

Ala Lys Glu Lys Gly Gly Glu Ala Leu Lys Gly Leu Thr Phe Val
                590                 595                 600

Ile Thr Gly Glu Leu Ser Arg Pro Arg Glu Glu Val Lys Ala Leu
                605                 610                 615

Leu Arg Arg Leu Gly Ala Lys Val Thr Asp Ser Val Ser Arg Lys
                620                 625                 630

Thr Ser Tyr Leu Val Val Gly Glu Asn Pro Gly Ser Lys Leu Glu
                635                 640                 645

Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr Glu Glu Glu Leu
                650                 655                 660

Tyr Arg Leu Leu Glu Ala Arg Thr Gly Lys Lys Ala Glu Glu Leu
                665                 670                 675

Val
```

Translation of the first 60 amino acids of this open reading frame (the thermophilic ligase) shows better than 50% homology to *E. coli* ligase [see Mol. Gen. Genet. 204:1 (1986)] suggesting that this long open reading frame represents the start of the *T. aquaticus* gene. From the genetic results with the BamHI fragments, one can conclude that the size of this ligase is between 400 and 1,100 amino acids in length. The purified protein has been reported to have a molecular weight of about 79,000 [see J. Biol. Chem. 259:10041 (1984)] which is within the limits of the genetic results found for the present invention. Given that clone pDZ**7** produces functional *T. aquaticus* ligase (that is it encodes the gene in its entirety), and given the DNA sequence of the amino terminus, the entire DNA sequence of the gene was determined using either manual or automated methods as described in the literature [see, for example, Proc. Natl. Acad. Sci. 84:4767 (1987); Proc. Natl. Acad. Sci. 86:4076 (1989); Science 239:487 (1987); Nature 321:674 (1986); Biotechniques 8:184 (1990); Proc. Natl. Acad. Sci. USA 85:5610 (1988); and Proc. Natl. Acad. Sci. USA 85:9436 (1988)].

Plasmids pDZ**2**, pDZ**3**, pDZ**6** or pDZ**7** may be used to construct further overproduction vectors using methods common to those skilled in biotechnology studies. This may include using promoters and ribosome binding sites as described above. For example, plasmid pDZ**7** (see FIG. **1**) may be linearized at its unique Asp**718** site, and excess nucleotides in front of the *T. aquaticus* ligase gene trimmed close to the ATG start codon by the use of Bal**31** or a combination of ExoIII and Mung Bean or S_1 Nuclease as described above. This may then be blunt end ligated to a natural enabling sequence (a promoter and translation start sequence) generated in a similar manner, or by a synthetic enabling sequence manufactured for this purpose. In addition, sequences external or internal to the *T. aquaticus* gene may be modified to remove potential RNA structures that may inhibit transcription or translation. These methods have been reported previously to affect overproduction of the thermophilic restriction endonuclease Taq I to greater than 30% of soluble *E. coli* proteins [see Gene 65:166 (1988)]. Alternatively, synthetic oligonucleotides may be synthesized such that the start of the *T. aquaticus* ligase gene is fused directly to an enabling sequence using PCR methods [see, for example, Biotechniques 8:178 (1990), Gene 77:51 (1989); and Nucl. Acids Res. 17:723 (1989)].

From the preceeding sequences, it can be seen that there is a Bgl II site corresponding to the nucleotides that code for amino acid residues **31**–**33**. With this information, a strong promoter with an optimal Shine-Dalgarno sequence could be inserted in front of this gene using PCR. Two minor caveats need to be considered: (1) attempts to PCR copy the entire gene (3 kb, high GC content) were not always successful, and (2) plasmid pDZ**7** had two Bam HI and Bgl II sites, one each within the ligase gene.

Plasmid pDZ**7** was partially digested with both Bam HI and Bgl II, the correct size smaller linear fragment separated from full length linear by electrophoresis, excised, and purified as described previously. Since Bam HI and Bgl II produce the same overhang (5' GATC), the linear fragment could be recircularized with T**4** ligase, and introduced into *E. coli* strain AK**53** via transformation. Several clones had deleted the 0.5 kb Bam HI/Bgl II fragment resulting in a 5.7 kb plasmid, and one such clone was designated pDZ**12**. Synthetic oligonucleotides **#66**, **#78**, **#85**, and **#94** were synthesized, to allow for fusion of pho A promoter [from plasmid pFBT**64**; see Gene 56:13 (1987)] and ribosome binding sequence to the start of the ligase gene using PCR [see Biotechniques 8:178 (1990); Gene 77:51 (1989); Gene 77:61 (1989); and Nucl. Acids Res.17:723 (1989)]. These clones are depicted in FIG. **9**, and are:

#66 19 mer; Pvu II site to T**7** promoter through phoA promoter, top strand of plasmid pFBT**64** (direction of TaqI endonuclease gene)(SEQ. ID. No. 9):

5' CTG GCT TAT CGA AAT TAA T 3'

#78 32 mer; 5' end complementary to start of *Thermus* ligase gene; 3' end complementary to Shine-Dalgarno side of pho A promoter, bottom strand of plasmid pFBT**64** (SEQ. ID. No. 10):

5' CCA GGG TCA TTT TAT TTT CTC CAT GTA CAA AT 3'

#85 33 mer; 5' end complementary to Shine-Dalgarno side of pho A promoter; 3' end complementary to start of *Thermus* ligase gene, top strand of plasmid pDZ**7** (direction of ligase gene)(SEQ. ID. No. 11):

5' CAT GGA GAA AAT AAA ATG ACC CTG GAA GAG GCG 3'

#94 18 mer; bottom strand of plasmid pDZ**7** corresponding to non-translated strand of amino acid residues **40** to **35** of ligase gene, downstream of Bgl II site at amino acid residues **33** to **31** (SEQ. ID. No. 12):

5' AAG CCG GTC GTA CTC GGC 3'

Briefly, this was accomplished in a single reaction tube in which 400 ng of primers **#66** and **#78** were added to 200 ng of Pst I/Pvu II digested pFBT**64** containing 50 μmoles of dATP, cCTP, CGTP, and dTTP each, and 2.5 units Amplitaq in 100 μl PCR buffer and cycled at 94° C. for 1 min, 55° C. for 2 min, 72° C. for 3 min with 3 sec. extension per cycle for 25 cycles as per the manufacturer's (Cetus, Emoryville, Calif.) protocol. A second reaction tube contained 400 ng of primers **#85** and **#94**, 200 ng of Eco RI/Bam HI digested pDZ**7**, in the same reaction buffer and enzyme, and incubated as above. The products of these reactions were shown to be the correct length as analyzed by gel electrophoresis. A third reaction tube contained 2 μl from each product, 400 ng primers **#66** and **#94** in the same reaction buffer and enzyme, and incubated as above. Primers were designed such that overlap between the two products would allow for PCR synthesis of the combined length fused product. The resultant fragment was extracted with phenol, n-butanol, and ethanol precipitated to remove Taq polymerase. The product PCR fragment was treated with Bgl II and Eco RI, electrophoresed in low melting agarose, and purified as described above. Meanwhile, the 2.7 kb Pst I-Bgl II ligase gene containing fragment from pDZ**12** and the 2.4 kb Pst I-Eco RI β-lactamase gene and origin containing fragment from pFBT**64** were purified. All three fragments were combined in a three way ligation and introduced into *E. coli* strain AK**53** via transformation. Several clones contained a 5.5 kb plasmid which overproduced ligase under pho A promoter control. One such plasmid has been designated pDZ**13**.

In reported studies in overproduction of the thermophilic restriction endonuclease Taq I to greater than 30% of soluble *E. coli* proteins [see Gene 65:166 (1988)], it was noticed that endonuclease yields were somewhat better if the β-lactamase gene was reversed, and hence transcribing in the opposite direction as the pho A promoter. To make a similar construction with the ligase gene according to the present invention, the 2.3 kb Pst I-Pvu II fragment from plasmid pFBLT**69** (which contains the β-lactamase in reverse orientation) was ligated to the 3.2 kb Pst I-Pvu II ligase gene containing fragment of plasmid pDZ**13**. The ligation mix was transformed into *E. coli* strain AK**53**, and several transformants were analyzed by restriction digests to confirm the orientation of β-lactamase gene. One such clone has been designated pDZ**15**. Production of ligase in pDZ**15** is as good as, if not slightly better than, pDZ**13**. The ligase enzyme appears to be somewhat sensitive to proteases, and the cells should be grown for no more than 9 hours after induction. Proteolytic products of the ligase gene may still have thermostable ligase activity (this has been demonstrated for Taq polymerase).

Thermophilic proteins may be substantially modified and still retain sufficient activity for use in the present invention. For example, it has been shown that deletion of approximately one-third of the coding sequence at the amino-terminus of Taq polymerase still produces a gene product that is active in polymerase activity [see J. Biol. Chem. 264:6427 (1989)]. Alternatively, another thermophilic protein, the restriction endonuclease Taq I, was shown to retain essentially full activity when amino acids were added to the amino-terminus (**+7**), the carboxy-terminus (**+38**), or at certain positions internally (from **+2** to **+34**) [see Gene 65:166 (1988)]. Thus, modification of the primary structure by deletion, n-terminus addition, c-terminus addition, internal addition or duplication, or alteration of the amino acids incorporated into the sequence during translation can be made without destroying the activity or thermostable nature of the protein. In addition, the availability of DNA encoding these sequences provides the opportunity to modify the codon sequence so as to generate mutein forms also having ligase activity. Such substitutions or other alterations result in novel proteins having amino acid sequence encoded by DNA falling within the scope of the present invention.

It will also be appreciated that other ligating proteins may be isolated by the process according to the present invention as exemplified in these examples. Different cell lines may be expected to produce ligases having different physical properties to that isolated from the *T. aquaticus* HB**8** strain used in the making of the present invention. Additionally, variations may exist due to genetic polymorphisms or cell-mediated modifications of the enzyme or its precursors. Furthermore, the amino acid sequence of a ligase so isolated may be modified by genetic techniques to produce ligases with altered biological activities and properties. The resultant DNA sequence may then be able to encode a protein having substantially the same amino acid sequence as *T. aquaticus* HB**8** ligase, but exhibiting a higher or lower level of activity. Such ligating proteins should also be considered to be within the scope of the present invention.

EXAMPLE VI

Purification of Ligase Enzyme

E. coli cells AK**53** containing plasmids pDZ**6** and pGP**1**–**2** (containing the T**7** RNA polymerase gene behind the lambda P_L promoter and under control of the temperature sensitive lambda repressor C_{1587}) [see Proc. Natl. Acad. Sci. USA 82:1074 (1985) and U.S. Pat. No. 4,795,699], were grown overnight at 32° C. on TY plates containing ampicillin at 50 μg/ml and kanamycin at 50 μg/ml to ensure maintenance of both plasmids. Fresh colonies were resuspended in 1 liter of sterile 50 mM Tris HCl buffer at pH 7.6 and containing 6 g NaCl, 25 g Bacto™-tryptone, 7.5 g yeast extract, 1 g glucose, 1.6 g casein amino acid hydrolysate, 50 μg/ml kanamycin and 50 μg/ml ampicillin, and grown at 32° C. in a 2 liter flask shaking at 200 rpm. When the $O.D._{550}$ reached between 0.8 and 1.0, synthesis of the T**7** polymerase was induced by shifting the cells to 42° C. for 30 to 40 minutes. Further synthesis of *E. coli* proteins were inhibited by the addition of 5 ml of 20 mg/ml rifampicin dissolved in methanol to a final concentration of 100 μg/ml. Under these conditions, only genes behind the T**7** promoter should be transcribed and hence translated. Cells were incubated for an additional 5 hours at 42° C.

Alternatively, *E. coli* cells AK**53** containing plasmids pDZ**15** (ligase under pho A promoter control) were grown overnight at 37° C. on TY plates containing ampicillin at 50 μg/ml. Fresh colonies were resuspended in 50 ml of fortified broth containing 50 μg/ml ampicillin and grown at 37° C. in a 500 ml flask shaking at 200 rpm in a G**76** benchtop shaker. When the $O.D._{500}$ reached between 0.65 and 0.85, 20 ml was diluted into 1 liter of MOPS media containing 0.2 mM K_2HPO_4 [see J. Bacteriology 119:736 (1974)] to induce the phoA promoter. Cells were grown at 37° C. in a 2 liter flask shaking at 200 rpm in a G**25** floor shaker for an additional 9 hours.

Following incubation, the cells were chilled in ice, harvested by centrifugation (5,000 rpm for 15 min), resuspended in 20 ml of water, transferred to 35 ml centrifuge tubes, recentrifuged (7,000 rpm for 6 min), and the pellet frozen until ready for protein isolation. After thawing, the pellet was resuspended in 20 ml of buffer A (20 mM Tris HCl buffer at pH 7.6 containing 1 mM EDTA) containing 10 mM 2-mercaptoethanol and 0.15 mM PMSF. After sonication (5×1 min at 50% power at 4° C.), the solution was centrifuged at 39,000×g for 60 min.

The enzyme has an estimated molecular weight of from 75,000 to 85,000 daltons when compared with a phosphorylase B standard assigned a molecular weight of 92,500 daltons.

Alternatively, 2 liters of pDZ**15** induced cells were harvested, sonicated, and debris cleared by centrifugation as described above.

The supernatant (40 ml) was brought to 300 mM KCl and passed through a 5 ml DEAE sephacel column to remove extraneous DNA using 70 ml buffer A containing 0.3 M KCl. The flowthrough fractions containing the ligase were combined, and treated at 65° C. for 20 minutes to irreversably heat denature many *E. coli* enzymes including endo or exonucleases. Denatured proteins were then removed by centrifugation at 39,000×g for 15 minutes, and the ligase enzyme precipitated from the supernatant by adding an equal volume of saturated $(NH_4)_2SO_4$ at room temperature for 30 minutes. The ammonium sulfate precipitate was harvested by centrifugation at 8,000 rpm in a clinical centrifuge, and resuspended in 4 ml of distilled water. Samples were dialyzed against buffer A, followed by buffer A containing 50 mM KCl. The dialized protein solution was applied to a 40 ml phosphocellulose column equilibrated with buffer A containing 50 mM KCl. After washing with 80 ml of the same buffer, the column was eluted with a 120 ml linear gradient of KCl (0.05 to 0.5 M) in buffer A. The enzyme eluted as a sharper peak from 0.25 to 0.35 M KCl. The protein migrates as two bands of apparent molecular weight approximately 81,000 (adenylated form) and 78,000 (non-adenylated form) and is about 98–99% pure as monitored by SDS-10% polyacrylamide gel electrophoresis. One can convert between the two forms by incubating 150 μg protein in ligase buffer containing either 25 μg nicked Salmon sperm DNA without NAD (resulting in the non-adenylated form), or in ligase buffer with 10 mM NAD (resulting in the adenylated form) for 30 min at 65° C. An equal volume of 20 mM Tris HCl pH 8.0 in 100% glycerol containing 1 mM EDTA, 2 mM dithiothreitol (DTT), and

200 μg/ml Bovine Serum Albumin (Fraction V) is added (final glycerol concentration is 50%), and enzyme stored at either −70° C. or −20° C. From 2 liters of cells, a final yield of 6 mg ligase in 16 ml storage buffer, at 625 nick closing units per microliter. This corresponds to a total of 10,000,000 units of enzyme, and a specific activity of 1,666,667 units/mg.

Since it is known that thermophilic proteins tend to be somewhat more hydrophobic than their mesophilic counterparts, addition of non-ionic detergents or other stabilizing agents may help in long term storage. Storage buffers may therefore include additional components such as glycerol (50%), sucrose (25%), protease inhibitors (0.5–1.0 mM PMSF, 10^{-7} M pepstatin A), salt (KCl, preferably at 100–500 mM), EDTA (0.1–1.0 mM) bovine serum albumin (100–500 μg/ml), gelatin, dithiothreitol (1–10 mM), and mercaptoethanol (1–10 mM). In addition, it is preferable that the storage buffer contain at least one non-ionic polymeric detergent. A partial listing of such detergents would include ethoxylated fatty alcohol ethers and lauryl ethers, ethoxylated alkyl phenols, polyethylene glycol monooleate compounds, and more particularly Triton X-100, NP-40, and Tween **20** at 0.1–0.5% vol/vol.

To assay for ligase activity, it is important to use a method that is not skewed by the melting temperature (T_m) of the substrates. For example, a 4 base cohesive end ligation is most efficient at a low temperature such as 4° C., well below the temperature optimum for T**4** ligase (which is 37° C.), and certainly below the temperature optimum of a thermophilic ligase. One assay method that should be consistent is the nick-closing assay in which circular plasmid DNA is randomly nicked in several places by DNaseI. The ability of ligase to close all these nicks and generate covalently closed circular DNA can be assayed by separating nicked circle from open circle DNA via electrophoresis in an agarose gel containing ethidium bromide. For example, the covalently closed circular form of plasmid pUC4KIXX [see Gene 37:111 (1985)] migrates faster than the linear form, and considerably faster than the nicked form on a 1% agarose gel containing 0.2 M glycine NaOH pH 8.5 0.1 mM EDTA, and 1 μg/ml ethidium bromide and run at 150 V for 1.5 hr in the same buffer.

EXAMPLE VII

Thermophilic Ligase Assay

Nicked pUC4KIXX DNA was generated by adding 3 μl of freshly diluted 1 μg/ml DNaseI to 5 μg DNA in 50 μl of 50 mM Tris HCl ph 8.0 buffer containing 10 mM $MgCl_2$, 1 mM EDTA, and 6 mM mercaptoethanol. The mixture was incubated at room temperature for 5 min, the DNase heat killed at 65° C. for 10 min, and the sample stored until used be freezing at −20° C. Under these conditions, about 90% of the DNA was in the nicked circular form, with about 5% in the linear and 5% in the covalently closed circular form.

Thermophilic ligase prepared as above was assayed by adding serial dilutions of ligase to 0.5 μg nicked pUC4KIXX in 20 μl of 20 mM Tris HCl pH 7.6 buffer containing 50 mM KCl, 10 mM $MgCl_2$, 1 mM EDTA, 10 mM NAD, 10 mM dithiothreitol, overlaying with a drop of mineral oil, and incubating at 65° C. for 15 min. As a control, T**4** ligase was assayed by adding serial dilutions of ligase to 0.5 μg nicked pUC4KIXX in 20 μl of 50 mM Tris HCl pH 8.0 buffer containing 10 mM $MgCl_2$, 1 mM EDTA, 1 mM ATP, 6 mM mercaptoethanol, and incubating at 37° C. for 15 min.

Reactions were terminated by the addition of 4 μl stop buffer containing 0.2 M EDTA, 50% glycerol, 1% SDS and 0.1% bromphenol blue, and the products were analyzed by gel electrophoresis as described above.

One nick closing unit of ligase is defined as the amount of ligase that circularizes 0.5 μg of nicked pUC4KIXX DNA under the buffer and time conditions set forth in the preceding example, such that addition of further ligase does not circularize additional DNA.

As a mini-prep procedure, *E. coli* cells AK**53** containing plasmids pDZ**15** (ligase under pho A promoter control) were grown overnight at 37° C. on TY plates containing ampicillin at 50 μg/ml. Fresh colonies were resuspended in 5 ml of fortified broth containing 50 μg/ml ampicillin, and grown at 37° C. When the $O.D._{550}$ reached between 0.65 and 0.85, 0.12 ml was diluted into 6 ml of MOPS media containing 0.2 mM K_2HPO_4 to induce the pho A promoter. Cells were incubated overnight at 37° C. (some proteolysis that occurs after prolonged incubation, so caution is advised in overgrowing induced cells). Cells were harvested in 1.5 ml microcentrifuge tubes, resuspended in 0.3 ml of 20 mM Tris HCL pH 7.6 containing 1 mM EDTA and 10 mM 2-mercaptoethanol, and sonicated 2×10 seconds. After clearing debris by centrifugation (12,000 rpm for 2 min.), the supernatant was treated at 65° C. for 20 min to irreversably heat denature many *E. coli* enzymes including the endo and exonucleaseses [see Gene 56:13 (1987)]. The denatured debris was removed by centrifugation and the supernatant assayed as described above. One microliter of this supernatant contained approximately 625 nick closing units of activity.

The *T. aquaticus* ligase preparation described in the preceding examples, as well as commercially available T**4** ligase, were shown to contain approximately 125 nick closing units per microliter. Thus, from 1 liter of *E. coli* cells overproducing *T. aquaticus* ligase, the process according to the present invention has purified approximately (800×125) 100,000 nick closing units of enzyme.

The thermophilic ligase prepared according to the preceding description has a number of valuable properties which makes it especially useful as an assay that both amplifies DNA and allows it to discriminate a single base substitution in a DNA sequence. The single most important property of this ligase allowing for these uses is that the ligase retains activity during repeated thermal denaturation/renaturation cycles thus allowing for the amplification of DNA without necessitating repeated addition of ligase. In addition, the ligase according to the present invention will ligate oligonucleotides of a length which is sufficient to assure their uniqueness in complex genomes at or near the T_m temperatures of 65° C., and will also accurately discriminate between exactly complementary and single based mismatched oligonucleotide sequences.

In the simpler of the two procedures developed as a result of cloning the thermophilic ligase DNA sequence, termed a ligase detection reaction (LDR), two oligonucleotide probes are allowed to hybridize to denatured DNA such that the 3' end of one is immediately adjacent to the 5' end of the other. The oligonucleotides are chosen to be sufficiently long (20 to 25 nucleotides) such that each will preferentially hybridize to its unique position in the human genome. A thermophilic ligase can then form a covalent phosphodiester bond between the two oligonucleotides, provided that the nucleotides at the junction are perfectly complementary to the target. The specificity of this nick-closing reaction is particularly enhanced by virtue of performing the ligation at or near the T_m of the two oligonucleotides for their target. Thus, a single base mismatch at the junction not only forms an imperfect double helix, but also destabilizes the hybrid at the higher temperature. Consequently, thermophilic ligase will efficiently link correctly base paired oligonucleotides and give near zero background ligation in the presence of the imperfectly matched sequences. Using LDR, the amount of product obtained in the ligation reaction can be increased in a linear fashion by repeated thermal cycling.

In the thermophilic ligase chain reaction according to the present invention, both strands serve as targets for oligonucleotide hybridization. By using an additional two oligonucleotides complementary to the opposite strand, the ligation products of one cycle become the targets for the next cycle of ligation as generally depicted in FIG. **2**. For each adjacent oligonucleotide pair, the diagnostic nucleotide is on the 3' side of the junction. Thus, aberrant target independent ligation of complementary oligonucleotides is avoided by use of temperatures near the T_m, and by taking advantage or the poor ligation efficiency of single base 3' overhangs. Using ligase chain reaction, the amount of product can be increased in an exponential fashion by repeated thermal cycling.

In order to test the potential of the thermophilic ligase chain reaction (LCR), the gene encoding human β globin was selected as an initial model system to test the technique of the present invention. Previous work has determined that the normal β^A allele and sickle β^S allele differ by a single A→T transversion of the second nucleotide in the sixth codon of the β globin gene, changing a glutamic acid residue into a valine in the hemoglobin β chain according to the following Table I (Oligonucleotide number **101** corresponds to SEQ. ID. No. 15; **102** corresponds to SEQ. ID. No. 14; **103** corresponds to SEQ. ID. No. 13; **104** corresponds to SEQ. ID. No. 24; **105** corresponds to SEQ. ID. No. 21; **106** corresponds to SEQ. ID. No. 22; **107** corresponds to SEQ. ID. No. 16;):

TABLE 1

Oligonucleotide	Sequence	
103	GTTTTT C ATG GTG CAC CTG ACG CCT GG	
102	GTTT C ATG GTG CAC CTG ACG CCT CT	
101	GT C ATG GTG CAC CTG ACG CCT CA	
107	G GAG AAG TCT GCC GTT ACT GCC	
β^A Globin	GACACC ATG GTG CAC CTG ACT CCT GAG GAG AAG TCT GCC GTT ACT GCC CTG	(5'-3')
	CTGTGG TAC CAC GTG GAC TGA GGA CTC CTC CTC AGA CGG CAA TGA CGG GAC	(3'-5')
109	TGG TAC CAC GTG GAC TGA GGA C	
104	TC CTC TTC AGA CGG CAA TGA CG TC	
105	AC CTC TTC AGA CGG CAA TCG CG TTTC	
106	CC CTC TTC AGA CGG CAA TCG CG TTTTTC	
β^A Globin	Met Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu	
β^S Globin	Met Val His Leu Thr Pro Val Glu Lys Ser Ala Val Thr Ala Leu	

In the following continuation of Table I, presents the oligonucleotide sequences listed in the preceding portion in their conventional 5'→3' orientation:

Sequence no.	Sequence 5'--->3'	size (mer)	Tm (° C.)
101	GT C ATG GTG CAC CTG ACT CCT GA	23	66
102	GTTT C ATG GTG CAC CTG ACT CCT GT	25	66
103	GTTTTT C ATG GTG CAC CTG ACT CCT GG	27	64
104	CT GC AGT GGC AGA CTT CTC CT	24	68
105	CTTT GC AGT GGC AGA CTT CTC CA	26	68
106	CTTTTT GC AGT AAC GGC AGA CTT CTC CC	28	66
107	G GAG AAG TCT GCC GTT ACT GCC	22	70
109	C AGG AGT CAG GTG CAC CAT GGT	22	70

Oligonucleotides containing the 3' nucleotide unique to each allele were synthesized with different length 5' tails (see Table I). Upon ligation to the invariant ^{32}P radiolabelled adjacent oligonucleotide, the individual products could be separated on a polyacrylamide denaturing gel and detected by autoradiography. Based upon these initial findings with autoradiography, subsequent assays were preformed using an automated, non-radioactive detection scheme in which the allele specific oligonucleotides were 5'-biotinylated for capture, and the invariant oligonucleotides 3'-tailed with digoxygenin. The label was then visualized in an ELISA format using anti-digoxigenin conjugated to alkaline phosphatase, and a colorimetric substrate for the enzyme.

As depicted in Table I, the nucleotide sequence and corresponding translated sequence of the oligonucleotides used in detecting β^A and β^S globin genes are depicted. Oligonucleotides **101** and **104** detect the β^A target, while **102** and **105** detect the β^S target when ligated to labelled oligonucleotides **107** and **104**, respectively. Oligonucleotides **103** and **106** were designed to assay the efficiency of ligation of G:T or G:A and C:A or C:T mismatches using β^A or β^S globin gene targets respectively. Oligonucleotides were designed with slightly different length tails to facilitate discrimination of various products when separated on a denaturing polyacrylamide gel. The tails which were not complementary to the target sequence, may be considered as being "reporter groups" for the individual sequence. Consequently, ligation of oligonucleotides **101**, **102**, or **103** to **107** gives lengths of 45, 47, or 49 nucleotides, respectively. For the complementary strand, ligation of oligonucleotides **104**, **105**, or **106** to **109** gives lengths of 46, 48, or 50 nucleotides, respectively. The oligonucleotides were also designed to have calculated T_m values of 66 to 70° C., which is just at or slightly above the ligation temperature.

In order to detect the ligation products, oligonucleotides **107** and **109** were 5'-end labelled with ^{32}P using T4 polynucleotide kinase and ^{32}P according to the following example.

EXAMPLE VIII

Radioactive Labelling

Oligonucleotide **107** (0.1 μg) was 5' end labelled in 20 μl 30 mM Tris HCl buffer at pH 8.0 containing 20 mM Tricine, 10 mM $MgCl_2$, 0.5 mM EDTA, 5 mM dithiothreitol, and 400 μCi of [^{32}P]ATP, by the addition of 15 units of T4 polynucleotide kinase. After incubation at 37° C. for 45 min, unlabelled ATP was added to 1 mM, and incubation was continued an additional 2 min at 37° C. The reaction was terminated by the addition of 0.5 μl 0.5 M EDTA, and kinase heat inactivated at 65° C. for 10 min. Unincorporated ^{32}P label was removed by chromatography with Sephadex G-25 pre-equilibrated with TE buffer. Specific activity ranged from 7×10^8 to 10×10^8 cpm/μg of oligonucleotide.

The specificity of the *T. aquaticus* thermophilic ligase according to the present invention for complementary vs. mismatched target was compared under both LDR and LCR conditions (see FIG. **3** and the following Table II). In the LDR series, two adjacent oligonucleotides were incubated with denatured target DNA and ligase, where the last nucleotide of the unlabelled oligonucleotide was either complemented or mismatched the target DNA. The oligonucleotides were designed with slightly different length tails to facilitate discrimination of various products by allowing them to be separated on a denaturing gel. Consequently, as disclosed earlier, ligation of oligonucleotide **101** (β^A allele), **102** (β^S allele), or **103** to labelled **107** gives lengths of 45, 47 or 49 nucleotides, respectively. For the complementary strand, ligation of oligonucleotides **104** (β^A allele), **105** (β^S allele), or **106** to labelled **109** gives lengths of 46, 48 or 50 nucleotides, respectively. The oligonucleotides were also designed to have a calculated T_m values of 66° C. to 70° C., that is just at or slightly above the ligation temperature. Thus, the specificity of ligating two oligonucleotides hybridized to target DNA with perfect complementarity (A:T) could be directly compared to each possible mismatch (A:A, T:T, G:A, G:T, C:A, or C:T). The methodology for determining specificity of ligation of these oligonucleotides in the presence of β^A or β^S globin gene target was determined as in the following example:

EXAMPLE IX

Determination of Specificity of Thermophilic Ligase

Labelled oligonucleotide (200,000 cpm; 0.28 ng; 40 fmoles) and unlabelled oligonucleotide (0.27 ng; 40 fmoles) were incubated in the presence of target DNA (1 fmole=6×10^8 molecules Taq I digested β^A or β^S globin plasmid) in 10 μl 20 mM Tris HCl buffer at pH 7.6 and containing 100 mM KCl, 10 mM $MgCl_2$, 1 mM EDTA, 10 mM NAD, 10 mM dithiothreitol, 4 μg Salmon sperm DNA, and 15 nick-closing units of the thermophilic ligase, and overlaid with a drop of mineral oil. The reactions were incubated at 94° C. for 1 min followed by 65° C. for 4 min, and this cycle was repeated between 5 and 30 times. The reactions were terminated by the addition of 8 μl formamide containing EDTA (10 mM), xylene cyanol (0.2%), and bromphenol blue (0.2%). Samples (4 μl) were denatured by boiling for 3 min prior to loading (40,000 cpm/lane) into the gel.

Products were separated by electrophoresis in which samples were loaded in groups of eight, run into the gel, and then the next set loaded, thereby accounting for the slightly slower mobility of the bands on the right side of the autoradiogram of FIG. **3**. Electrophoresis was in a 10% polyacrylamide gel containing 7 M urea in a buffer of 100 mM Tris borate pH 8.9 and 1 mM EDTA, for 2 hrs at 60 W constant power.

After removing the urea by soaking for 10 min in 10% acetic acid followed by a second soak of 5 min in water, the gels were dried onto Whatman 3 mm paper and autoradiographed overnight at −70° C. on Kodak XAR-5 film (with or without Du Pont Cronex lighting plus intensifying screen). Bands from 20 cycles were excised from the gels and assayed for radioactivity. The results are given in Table II.

TABLE II

Quantitation of complementary and mismatched LDR and LCR bands from 20 cycle LDR and 30 cycle LCR experiments described in Example IX and depicted in FIG. 3 were excised from gels and assayed for radioactivity. Percentage product formed = cpm in product band/cpm in starting oligonucleotide band. Percentage mismatched/complementary = cpm in band of mismatched oligonucleotides/cpm in band of complementary oligonucleotide using the same target DNA, and gives an indication of the noise to signal ratio. LDR amplification was performed using 6 × 10^8 target molecules or 1 femtomole; LCR amplification was performed using 6 × 10^6 target molecules or 10 attomoles.

	Oligo base: target base	Product formed (%)	mismatched/ complementary (%)
LDR	A:T	21.5	
	T:A	13.2	
	T:A	17.9	
	A:T	12.4	
	A:A	<0.1	<0.4
	T:T	0.12	0.7
	T:T	0.16	1.0
	A:A	<0.1	<0.4

TABLE II-continued

Quantitation of complementary and mismatched LDR and LCR bands from 20 cycle LDR and 30 cycle LCR experiments described in Example IX and depicted in FIG. 3 were excised from gels and assayed for radioactivity. Percentage product formed = cpm in product band/cpm in starting oligonucleotide band. Percentage mismatched/complementary = cpm in band of mismatched oligonucleotides/cpm in band of complementary oligonucleotide using the same target DNA, and gives an indication of the noise to signal ratio. LDR amplification was performed using 6 × 10^8 target molecules or 1 femtomole; LCR amplification was performed using 6 × 10^6 target molecules or 10 attomoles.

	Oligo base: target base	Product formed (%)	mismatched/ complementary (%)
	G:T	0.30	1.4
	C:T	<0.1	<0.4
	G:A	<0.1	<0.4
	C:A	<0.1	<0.4
LCR	A:T, T:A	41.4	
	T:A, A:T	10.4	
	A:A, T:T	0.45	1.1
	T:T, A:A	<0.05	<0.2
	G:T, CA	0.51	1.3
	G:A, C:T	<0.05	<0.2

Thus, the thermophilic *T. aquaticus* ligase was shown to discriminate complementary from mismatched oligonucleotide sequences for all possible mismatched base pairs in LDR assays. Under both competition and individual ligation experiments (at varying salt concentrations), the worst case mismatch ligations were 1.5 to 1.0% (see Table II, G:T and T:T), while others were 0.4% to <0.1% (see Table II, A:A, C:T, G:A and C:A) of the products formed with complementary base pairs (A:T). This is substantially better than reported (using radioactive detection) for the mesophilic T4 ligase of *E. coli* [see Gene 76:245 (1989)].

In the LCR amplification/detection series of experiments, two adjacent oligonucleotides were incubated with denatured target DNA and ligase, as well as with the complementary set of oligonucleotides. Under these conditions, the 3' nucleotide of the unlabelled diagnostic oligonucleotide either complemented or mismatched the target DNA, but always complemented its unlabelled counterpart, i.e. A:T for **101** and **104**, T:A for **102** and **105**, and G:C for **103** and **106**. Thus, an initial "incorrect" ligation of a mismatched oligonucleotide would subsequently be amplified with the same efficiency as a correct ligation. Samples contained pairs of unlabelled oligonucleotides (β^A allele specific **101** and **104**, β^S allele specific **102** and **105**, or **103** and **106**) with the complementary and adjacent pairs of labelled oligonucleotides, **107** and **109**. These labelled and unlabelled oligonucleotides were incubated in the presence of ligase and 10 attomoles of target DNA (100 fold less target DNA than for LDR) for 20 or 30 cycles as in Example IX,. The resulting bands are depicted in the left portion of FIG. **3** and the lower half of Table II.

As can be seen in FIG. **3** and Table II, the thermophilic ligase according to the present invention was capable of discriminating complementary from mismatched oligonucleotide sequences for all possible mismatched base pairs in LCR assays. Under both competition and individual ligation experiments the worse case mismatch ligations were from 1.3% to 0.6% (G:T, C:A and A:A, T:T), while others were <0.2% (T:T, A:A and G:A, C:T) of the products formed with complementary base pairs (A:T, T:A). LCR, using thermophilic ligase according to the present invention, is thus the only method which can both amplify and detect single base mismatches with high signal to noise ratios [see Genomics 4:560 (1989)]. Thus, by utilizing LCR one can detect the difference between a single base mismatch such as occurs between β^A and β^S, and use the results of this assay as a diagnostic for the normal, the carrier, or the diseased patient.

When the entire set of experiments described above were repeated using buffer containing 150 mM instead of 100 mM KCl, the results were essentially the same as in FIG. **3** and tabulated in Table II, with ligation of mismatch oligonucleotides for LDR ranging from 0.6% to <0.3% and for LCR ranging from 1.7% to <0.3% of the exactly complementary products. Thus, the exquisite discrimination between matched and mismatched oligonuclootides appears not to be critically dependent upon salt conditions.

Alternatively, a different procedure based on phosphatase may also be used. The LCR or LDR reaction may be performed in a 10 μl volume under mineral oil. To this is added 50 μl of 10 mM Tris HCl pH 7.6 containing 0.5 units of Bacterial Alkaline Phosphatase (BAP), and 10 mM $MgCl_2$, and the incubation continued at 65° C. for 2 hrs (note that the ligase enzyme is not killed under these conditions). The 5' end label on an oligonucleotide that has become covalently linked is no longer susceptible to BAP. Ligated product is separated from monophosphate by the addition of 20 μl of 10 mg/ml sonicated salmon sperm DNA as a carrier and precipitated with 20 μl of 50% TCA. After centrifugation for 5 min at 12,000 rpm, the supernatant is removed, and the ration of pellet to pellet + supernatant gives the percentage of product formed. A similar assay has been used with Taq I endonuclease, and the experimental error for positive and negative controls is around 1–2%.

Use of the thermophilic ligase according to the present invention obviates the need to carefully titrate both salt and enzyme concentration as required for mesophilic ligases. The data from this series of experiments is tabulated in the following Table III.

TABLE III

Quantitation of complementary and mismatched LDR and LCR bands, at 100 and 150 mM KCl concentrations, from 20 cycle LDR and 30 cycle LCR experiments described in Example IX and depicted in FIG. 3. LDR amplification was performed using 6 × 10^8 target molecules or 1 femtomole; LCR amplification was performed using 6 × 10^6 target molecules or 10 attomoles. The mismatched/complementary gives an indication of the noise to signal ratio.

	Oligo base: target	Product formed (%) [KCl] (mM)		mismatched/ complementary (%) [KCl] (mM)	
	base	100	150	100	150
LDR	A:T	21.5	23.2		
	T:A	13.2	17.2		
	T:A	17.9	12.8		
	A:T	12.4	11.7		
	A:A	<0.1	<0.2	<0.4	<0.3
	T:T	0.12	0.21	0.7	0.3
	T:T	0.16	0.30	1.0	0.6
	A:A	<0.1	<0.2	<0.4	<0.3
	G:T	0.30	0.25	1.4	0.4
	C:T	<0.1	<0.2	<0.4	<0.3
	G:A	<0.1	0.25	<0.4	0.4
	C:A	<0.1	0.20	<0.4	0.3
LCR	A:T, T:A	41.4	14.2		
	T:A, A:T	10.4	18.5		
	A:A, T:T	0.45	0.09	1.1	0.6
	T:T, A:A	<0.05	<0.05	<0.2	0.3

TABLE III-continued

Quantitation of complementary and mismatched LDR and LCR bands, at 100 and 150 mM KCl concentrations, from 20 cycle LDR and 30 cycle LCR experiments described in Example IX and depicted in FIG. 3. LDR amplification was performed using 6 × 10^8 target molecules or 1 femtomole; LCR amplification was performed using 6 × 10^6 target molecules or 10 attomoles. The mismatched/complementary gives an indication of the noise to signal ratio.

Oligo base: target	Product formed (%) [KCl] (mM)		mismatched/ complementary (%) [KCl] (mM)	
base	100	150	100	150
G:T, C:A	0.51	0.24	1.3	1.7
G:A, C:T	<0.05	<0.1	<0.2	<0.7

LCR and LDR specificity was tested using both β^A and β^S specific oligonucleotides in direct competition for ligation to the invarient labelled oligonucleotides. Using target DNA (β^A, β^S, and an equimolar ratio of β^A and β^S) ranging from 1 femtomole to 1 attomole, thermophilic ligase specifically formed the correct product(s) in each case; no background incorrect ligation product was observed when only one target allele was present). However, the efficiency of forming the β^S specific products is somewhat less than forming the β^A products, and after 20 cycles of amplification, the β^S specific products were approximately one-third of the BA specific products as quantitated by assaying excised products for radioactivity. Hence a direct competition assay, wherein two oligonucleotides are differentially labelled (for example with fluorescent groups) to quantitate the relative initial concentrations of each target sequence allele will require careful titrations for each allele.

The specificity of LCR DNA amplification with sub-attomole quantities of target DNA was also examined. The extent of LCR DNA amplification was determined in the presence of target DNA ranging from 100 attomoles (6×10^7 molecules) to less than one molecule per tube. Reactions were incubated for 20 or 30 cycles, and products separated and quantitated as depicted in FIG. **4** and the following table IV.

TABLE IV

Quantitation of LCR amplification. Bands from 30 cycle LCR experiments were excised from the gels and assayed for radioactivity. At higher target concentration, DNA amplification was essentially complete after 20 cycles; slightly imprecise excision of 30 cycle bands from this portion of the gel probably accounts for product formed values in excess of 100%. Percentage product formed = cpm in product band/cpm in starting oligonucleotide band; Amplification = No. of product molecules formed/No. of target molecules

Target Molecules	Product formed (%)	Amplification
6 × 10^7	134	
2 × 10^7	96	
6 × 10^6	107	
2 × 10^6	78	
6 × 10^5	85	
2 × 10^5	48	5.8 × 10^4
6 × 10^4	25	1.0 × 10^5
2 × 10^4	4.5	5.4 × 10^4
6 × 10^3	2.3	9.2 × 10^4
2 × 10^3	0.36	4.3 × 10^4
6 × 10^2	0.18	7.2 × 10^4
2 × 10^2	0.14	1.7 × 10^5
60	<0.05	
20	<0.05	
6	<0.05	
2	<0.05	
0	<0.05	

In the absence of target, no background signal was detected when carrier salmon sperm DNA (4 μg) was present as seen in FIG. **4**. At higher initial target concentrations, DNA amplification was essentially complete after 20 cycles, while at lower initial target concentrations substantially more product is formed with additional amplification cycles. Under these conditions, 200 molecules of initial target DNA could easily be detected after 30 cycles.

The thermostable nature of the enzyme is readily apparent in FIG. **4**. By comparing the amount of product formed after 20 cycles to that formed after 30 cycles, it is apparent that at the lower target DNA concentrations additional product is formed after more cycles (see especially 2×10^4 to 2×10^2 target DNA molecules). In other words, the enzyme still has activity after 20 cycles of 94° C. for 1 minute followed by 65° C. for 4 minutes.

Thus, *T. aquaticus* ligase retains the ability to catalyze formation of a phosphodiester bond between two adjacent oligonucleotides hybridized to a complementary strand of DNA at a temperature in the range of about 50° C. to about 85° C. after repeated exposure to temperatures that denature DNA, namely in the range of about 105° C. for about 0.25 minutes to about 4 minutes.

Hence, the specific amplification of a nucleic acid test substance of known nucleotide sequence using LCR requires: (1) two adjacent oligonucleotides complementary to and in molar excess of the target sequence nucleic acid, and having no mismatch to the target sequence nucleic acid at the junction of the adjacent oligonucleotides; (2) a second set of adjacent oligonucleotides complementary to the first set of adjacent oligonucleotides, complementary to and in molar excess of the target sequence nucleic acid, and having no mismatch to the target sequence nucleic acid at the junction of this second set of adjacent oligonucleotides; (3) a thermostable ligase which does not become irreversibly denatured and lose its catalytic ability when subjected to temperatures of from about 50° C. to about 105° C.; and (4) subjecting this ligase mixture to repeated temperature cycles which comprises a first temperature to denature the DNA (in a range of about 90° C. to about 105° C.), and a second temperature to allow for hybridization/ligation (in a range of about 50° C. to about 85° C.). In the amplification of β^A globin allele described above, the components were (1) oligonucleotides **101** and **107**; (2) oligonucleotides **104** and **109**; (3) *T. aquaticus* ligase; and (4) 30 temperature cycles of 94° C. for 1 minute followed by 65° C. for 4 minutes.

In FIG. **4**, bands of 45 and 46 nucleotides correspond to ligation products of the coding and complementary β^A globin oligonucleotides. Lower molecular weight products correspond to ligation of deletion oligonucleotides present in the initial ligation reaction. Since samples were loaded in groups of eight, the right side of the autoradiogram gives the appearance of slower migration.

To further test the ability of ligase to discriminate between complementary and mismatched oligonucleotides, an LCR experiment was performed in the presence and absence of oligonucleotides which would give G–T and C-A mismatches in accordance with the following example which not only shows DNA amplification, but also supports the thermostable nature of the enzyme found in Example IX.

EXAMPLE X

One set of experiments contained 40 fmoles each of unlabelled **101** and **104** oligonucleotides, while the second set had in addition 40 fmoles of unlabelled **103** and **106** oligonucleotides. Both sets contained 40 fmoles each of labelled **107** and **109**. Labelled oligonucleotides (200,000 cpm; 0.28 ng; 40 fmoles) and unlabelled oligonucleotides (0.27 ng; 40 fmoles) were incubated in the presence of target DNA, ranging from 100 attomoles (6×10^7 molecules) to 0.01 attomoles (6×10^3 molecules) of Taq I digested β^A or β^S globin plasmid. Incubation was carried out in 10 μl 20 mM Tris-HCl, ph 7.6 buffer containing 100 mM $MgCl_2$, 1 mM EDTA, 10 mM NAD, 10 mM dithiothreitol, 4 μg Salmon sperm DNA, and 15 nick-closing units of *T. aquaticus* ligase, and overlaid with a drop of mineral oil. Reactions were incubated at 94° C. for 1 min followed by 65° C. for 4 min, and this cycle was repeated 20 or 30 times.

The resulting samples were electrophoresed, gel autoradiographed overnight with the aid of a Cronex intensifying screen and the bands counted. The bands from the autoradiographed gel are depicted in FIG. **4**, and the quantitation of LCR amplification tabulated in the following Table V.

TABLE V

Quantitation of LCR amplification the presence or absence of mismatched competitor molecules.

	Complementary Oligonucleotides (101, 104) (A:T, T:A)		Complementary & Mismatched Oligonucleotides (101, 104 & 103, 106) (A:T, T:A & G:T, CA)		
Target molecules	Product formed	Amplification	Product formed	Amplification	Mismatched/ Complementary
$6 \times 10^{7\,(\beta A)}$	114		93		1.0
2×10^7	93		95		1.8
6×10^6	102		93		0.5
2×10^6	90		67		0.5
6×10^5	51		46		
2×10^5	31	3.7×10^4	23	2.8×10^4	
6×10^4	17	6.8×10^4	9.3	3.7×10^4	
2×10^4	8.6	1.0×10^5	2.9	3.5×10^4	
6×10^3	3.2	1.3×10^5	0.8	3.4×10^4	
0	<0.1		<0.1		
$6 \times 10^{7\,(\beta S)}$	2.1		1.5		

At high target concentrations, sufficient mismatched product was produced to be visualized (as in FIG. **4**), the quantity of mismatched product ranging from 1.8% to 0.5% of the complementary product. Use of an excess of mismatched target DNA (β^S instead of β^A globin DNA at 6×10^7 molecules per tube) gave only 2.1% and 1.5% product. The same amount of product may be formed when using three to ten thousand fold less complementary target DNA. Based upon this, the signal from correctly paired ligation products is 50 to 500 fold higher than mismatched products under competition or individual LCR ligation conditions.

At low target concentrations, the extent of DNA amplification ranged from 3.7×10^4 to 1.7×10^5 (see Tables IV and V). Assuming the efficiency of ligation is the same in each cycle, the average amplification per cycle is between 40 and 50%.

The efficiency per cycle could, of course, be potentially enhanced by altering buffer conditions, enzyme concentration, or thermal cycling times and temperatures—all within the capabilities of those skilled in the art. It has, for example, been shown that the ligation efficiency of thermophilic ligase (and other ligases) may be enhanced by altering buffer compositions, such as using NH_4Cl, HEPES, polyamines such as spermidine, or polyethylene glycols [see J. Biol. Chem 259:10041 (1984), and J. Biochem. 100:123 (1986)]. Varying the amounts of each component in the currently used buffer and either supplementing or exchanging one or more components with, but not limited to, the chemical and biological components listed above, are among the methods of improving LCR that are straight forward for those skilled in the art. One skilled in the art can also easily vary the cycling times and temperatures. For example, at later time points, the majority of target present is oligonucleotide product from a previous LCR reaction. These oligonucleotides are short (preferably but not limited to 40–60 mers) and may melt more rapidly, allowing more rapid cycling. In the present invention, successful ligase chain reactions have been completed for 30 and 40 cycles under cycling conditions of 94° C. for 0.5 minutes followed by 65° C. for 2 minutes (half the time of the 1 minute at 94° C. and 4 minutes at 65° C. cycle time for the preferred ligase chain reaction conditions). Both the ligation temperature and the DNA denaturing temperatures may be varied with respect to actual degree, duration, and number of repeated cycles. Optimal conditions must maximize the amount of product formed in the presence of perfectly complementary target DNA, while minimizing the amount of incorrect product formed in the presence of mismatched target DNA or in the absence of complementary target DNA.

Utilizing these findings, a method for the detection of specific sequences of oligonucleotides in clinical samples was developed. The source of the sample may be any material or substance which comprises nucleic acid. The nucleic acid need not be a naturally occurring nucleic acid, but may be synthesized by chemical, enzymatic, or biological means and may have other than naturally occurring purines and pyrimidines. The source of the clinical sample may be cellular or non-cellular, and may be derived from such physiological media as blood, serum, plasma, breast milk, stool, pus, tissue scrapings, washings, urine, or the like. Furthermore, the sample may be associated with a set or subset of cells, such as neoplastic cells, lymphocytes (for example, T-cells or B-cells, monocytes, neutrophils, etc); may include pathogens including viruses, bacteria, mycoplasma, fungi, protozoa, etc.; may include constructs, etc. or RNA, such as messenger RNA, transfer RNA, ribosomal RNA, viruses, or the like; and it may involve structural genes, untranslated regions, regulatory regions, introns, exons, or the like. In addition, the detection may be for a wide variety of purposes such as, for example, the diagnosis of a potential or actual disease state in plant or animal species, as well as the detection of sets or subsets of pathogens, the monitoring of genetic engineering, or the like.

One such method for which the present invention may be used (and which clearly demonstrates the feasibility of direct

LCR allelic detection from blood samples without the need for prior PCR amplification) is embodied, for example, in the detection of β-globin alleles in human genomic DNA. Based upon the high level of DNA amplification, the allele specific LCR detection of DNA was examined from blood collected from normal ($\beta^A\beta^A$), carrier ($\beta^A\beta^S$), and sickle cell ($\beta^S\beta^S$) individuals as more fully described in the following example:

EXAMPLE XI

Detection of β-Globin Alleles in Human Genomic DNA

Human genomic DNA was isolated from 0.5 ml whole blood [see *PCR Technology,* H. A. Erlich editor, Stockton Press 1989) pg 36]. Whole blood (0.5 ml) was mixed with an equal volume of lysis buffer (10 mM Tris-HCl, pH 7.6, containing 5 mM $MgCl_2$ and 0.32 M sucrose). After a brief centrifugation (1 min at 12,000 rpm in an eppendorf desktop centrifuge), the supernatant was very carefully removed, leaving 0.15 to 0.2 ml of supernatant and loosely pelleted nuclei. The pellet was resuspended with vortexing in an additional 0.5 ml lysis buffer, nuclei pelleted and the supernatant removed as above. This step was repeated three or four times until the supernatant was clear or just barely pink. After removal of the final supernatant (again leaving about 0.15 to 0.2 ml), 0.25 ml of LCR DNA Buffer containing non-ionic detergents (20 mM Tris-HCl, pH 7.6, containing 2 mM EDTA and 0.45% each of non-ionic detergents NP40 and Tween **20**) was added. Any excess RNA was digested by the addition of 2 μl of 4 mg/ml heat treated RNase A for 15 min at 37° C. Any proteins were digested by the addition of 5 μl of 10 mg/ml freshly made Proteinase K and incubation at 50° C. for 1 to 2 hours. Proteinase K and RNase A were removed by sequential extractions with phenol, phenol/chloroform, chloroform, n-butanol (2X) and the nucleic acid recovered by precipitation with ethanol. Samples were boiled for 5 min prior to use in LCR assays.

Each isolated human genomic DNA was tested in two reaction mixtures, the first testing for the presence of the normal β^A allele, and the second testing for the presence of the sickle β^S allele. The first reaction mixture contained β^A test oligonucleotides **101** and **104** (0.27 ng or 40 fmoles each), labelled oligonucleotides (**107** and **109**; 200,000 cpm (0.28 ng or 40 fmoles each), genomic DNA (corresponding to 10 μl of blood, or about 6×10^4 nucleated cells) in 10 μl 20 mM Tris-HCl buffer, pH 7.6, containing 100 mM KCl, 10 mM $MgCl_2$, 1 mM EDTA, 10 mM NAD, 10 mM dithiothreitol, and 15 nick-closing units of *T. aquaticus* ligase, and overlaid with a drop of mineral oil. The second reaction mixture contained β^S test oligonucleotides **102** and **105** (0.27 ng or 40 fmoles each), labelled oligonucleotides **107** and **109** (200,000 cpm or 0.28 ng or 40 fmoles each), genomic DNA corresponding to 10 μl of blood or about 6×10^4 nucleated cells) in 10 μl 20 mM Tris-HCl buffer, pH 7.6 and containing 100 mM KCl, 10 mM $MgCl_2$, 1 mM EDTA, 10 mM NAD, 10 mM dithiothreitol, and 15 nick-closing units of *T. aquaticus* ligase, and overlaid with a drop of mineral oil.

Both reaction mixtures were incubated at 94° C. for 1 min followed by 65° C. for 4 min, and this cycle was repeated 20 to 30 times. Reactions were terminated by the addition of 8 μl formamide containing EDTA (10 mM), xylene cyanol (0.2%), and bromphenol blue (0.2%).

Samples (4 μl) were denatured by boiling for three min prior to loading (40,000 cpm/lane). Electrophoresis was in a 10% polyacrylamide gel containing 7 M urea in a buffer of 100 mM Tris borate at ph 8.9 and 1 mM EDTA, for 2 hours at 60 Watt constant power. After removing the urea (10 min soak in 10% acetic acid, followed by 5 min soak in H_2O). Gels were then dried onto Whatman 3 mm paper and autoradiographed overnight at −70° C. on Kodak XAR-5 film with a DuPont Cronex intensifying screen. Ligation products of 45 and 46, or 47 and 48 nucleotides indicate the presence of the β^A or β^S globin gene, respectively. As noted with plasmid derived target DNA, the efficiency of ligation (and hence detection) is somewhat less for the β^S than the β^A specific oligonucleotides.

FIG. **5** is an autoradiogram showing the detection of β-globin alleles in human genomic DNA made in accordance with the proceeding example. Ligation products of 45 and 46, or 47 and 48 nucleotides indicate the presence of the β^A or β^S globin gene, respectively. Thus, with target DNA corresponding to 10 μl of blood, β^A and β^S alleles could be readily detected using allele specific LCR.

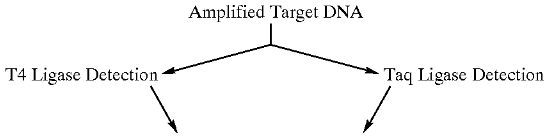
Hence, the successful detection of a biologically derived nucleic acid test substance, which has a known normal nucleotide sequence and a known possible mutation at at least one target nucleotide position in the sequence, requires (1) a first reaction mixture comprising two sets of adjacent oligonucleotides complementary to each other, complementary to the target sequence nucleic acid, wherein there is at least one mismatched base pair to the mutant target sequence nucleic acid, but not to the normal target sequence nucleic acid at the junction of the adjacent oligonucleotides; (2) a second reaction mixture comprising two sets of adjacent oligonucleotides complementary to each other, complementary to the target sequence nucleic acid, wherein there is at least one mismatched base pair to the normal target sequence DNA, but not to the mutant target sequence nucleic acid at the junction of the adjacent oligonucleotides; (3) a thermostable ligase which does not become irreversibly denatured and lose its catalytic ability when subjected to temperatures of from about 50° C. to about 105° C.; and (4) subjecting these ligase mixtures to repeated temperature cycle which comprises a first temperature to denature the DNA (in a range of about 90° C. to about 105° C.), and a second temperature to allow for hybridization/ligation (in the range of about 50° C. to about 85° C.)—this also allows adjacent oligonucleotides in each reaction mixture to become possibly covalently linked; (5) separating the test substance and any unlinked test oligonucleotides from covalently linked oligonucleotide product (if formed); and (6) detecting the presence or absence of covalently linked oligonucleotides in each reaction mixture whereby the presence of covalently linked oligonucleotide product in the first reaction mixture indicates the presence of normal target sequence and the presence of covalently linked oligonucleotide product in the second reaction mixture indicates the presence of mutant target sequence. In the detection of β^A and β^S globin alleles described above, the components were (1) oligonucteotides **101**, **104**, **107** and **109**; (2) oligonucleotides **102**, **105**, **107** and **109**; (3) *T. aquaticus* ligase; (4) 30 temperature cycles of 94° C. for 1 min followed by 65° C. for 4 min; (5) denaturing nucleic acids by boiling in 45% formamide and separating on a sequencing gel; and (6) autoradiographing of the gel.

This clearly demonstrates the feasibility of direct LCR allelic detection from blood samples according to the present invention without the need for PCR amplification.

As noted with plasmid derived target DNA, the efficiency of ligation (and hence detection) is somewhat less for the β^S than the β^A specific oligonucleotides. After 30 cycles of amplification, β^S specific products were approximately one-third of β^A specific products, as quantitated by assaying excised products for radioactivity. These differences may be a function of the exact nucleotide sequence at the ligation junction, or the particular oligonucleotides (with differing 5' tails) used in the LCR experiments. However, the present invention still allows for a direct competition assay where two oligonucleotides are differentially labelled (for example with fluorescent groups or, in this case, with different length tails) to determine the presence or absence of either allele in a reaction mixture. In the generalized form, the method according to the present invention allows one to assay two alleles in the same vessel, providing the sets of oligonucleotides containing at least one mismatched base pair to the mutant target sequence nucleic acid, but not to the normal target sequence nucleic acid at the junction of the adjacent oligonucleotides, are labelled with one set of labels, and the oligonucleotides containing at least one mismatched base pair to the normal target sequence nucleic acid, but not to the mutant target sequence nucleic acid at the junction of the adjacent oligonucleotides, are labelled with a different label.

In a comparable non-radioactive assay, as depicted in FIG. **6**, a minimum of two oligonucleotide probes are synthesized and modified for particular functions in the ligation assay. One probe contains a hook that permits the capture of the oligonucleotide following ligation. An example of such a hook is biotin which can be captured by streptavidin or avidin bound to appropriate supports. The other probe has a reporter group. Although a variety of reporter groups, both radioisotopic and non-radioactive, are available and can be used with the assay according to the present invention, such as fluorophores or luminescent moieties, the currently preferred reporter is one which may participate in an ELISA (enzyme-linked immuno sorbent assay). More specifically, FIG. **6** depicts a schematic diagram of an ELISA based oligonucleotide ligation assay in which biotinylated (B) and digoxigenin-labelled (D) oligonucleotides are hybridized with a DNA target in the presence of ligase (arrow). Biotinylated oligonucleotides are captured on streptavidin (SA) coated within the wells of microtiter plates. The wells are washed to remove unbound oligonucleotides, and alkaline phosphatase (AP) conjugated anti-digoxigenin antibodies (D) are added to the wells. Following an incubation and wash cycle, alkaline phosphatase substrate (S) is added, and digoxigenin detected by the production of a color product.

The non-radiolabelled assay according to the present invention consists of several steps: (1) preparation of the DNA target; (2) denaturation and hybridization of the modified oligonucleotide probes; (3) ligation; (4) capture of the biotinylated probe; (5) washing to remove free nonbiotinylated oligonucleotides and target; (6) addition of alkaline phosphatase conjugated anti-digoxigenin antibodies; (7) washing to removed unbound antibody; (8) addition of alkaline phosphatase substrate; and (9) spectrophotometric analysis. The following flow chart details the general procedure (which has automated on a modified Biomek 1000 workstation instrument) by which a non-radiolabelled assay according to the present invention can be conducted:

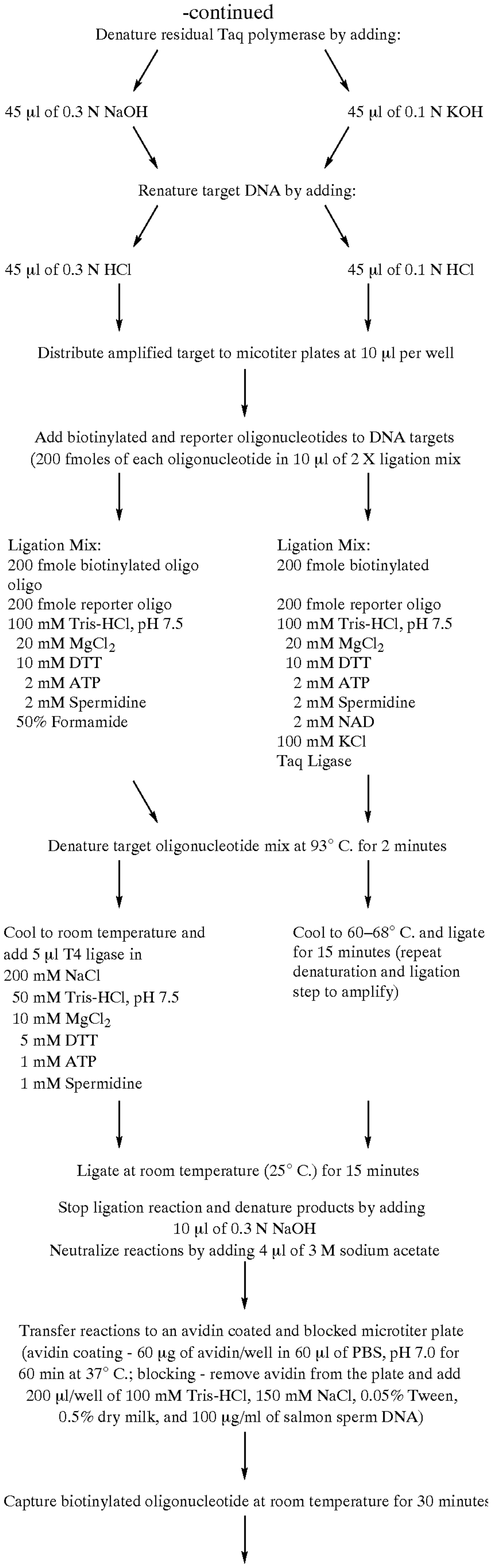


Amplified Target DNA

T4 Ligase Detection

Taq Ligase Detection

-continued



Denature residual Taq polymerase by adding:

45 μl of 0.3 N NaOH

45 μl of 0.1 N KOH

Renature target DNA by adding:

45 μl of 0.3 N HCl

45 μl of 0.1 N HCl

Distribute amplified target to micotiter plates at 10 μl per well

Add biotinylated and reporter oligonucleotides to DNA targets (200 fmoles of each oligonucleotide in 10 μl of 2 X ligation mix

Ligation Mix:	Ligation Mix:
200 fmole biotinylated oligo oligo	200 fmole biotinylated
200 fmole reporter oligo	200 fmole reporter oligo
100 mM Tris-HCl, pH 7.5	100 mM Tris-HCl, pH 7.5
20 mM $MgCl_2$	20 mM $MgCl_2$
10 mM DTT	10 mM DTT
2 mM ATP	2 mM ATP
2 mM Spermidine	2 mM Spermidine
50% Formamide	2 mM NAD
	100 mM KCl
	Taq Ligase

Denature target oligonucleotide mix at 93° C. for 2 minutes

Cool to room temperature and add 5 μl T4 ligase in
200 mM NaCl
50 mM Tris-HCl, pH 7.5
10 mM $MgCl_2$
5 mM DTT
1 mM ATP
1 mM Spermidine

Cool to 60–68° C. and ligate for 15 minutes (repeat denaturation and ligation step to amplify)

Ligate at room temperature (25° C.) for 15 minutes

Stop ligation reaction and denature products by adding 10 μl of 0.3 N NaOH

Neutralize reactions by adding 4 μl of 3 M sodium acetate

Transfer reactions to an avidin coated and blocked microtiter plate (avidin coating - 60 μg of avidin/well in 60 μl of PBS, pH 7.0 for 60 min at 37° C.; blocking - remove avidin from the plate and add 200 μl/well of 100 mM Tris-HCl, 150 mM NaCl, 0.05% Tween, 0.5% dry milk, and 100 μg/ml of salmon sperm DNA)

Capture biotinylated oligonucleotide at room temperature for 30 minutes

-continued

Wash plate to remove unbound oligonucleotides and targets with (1) 100 mM Tris-HCl, pH 7.5, in 150 mM NaCl in 0.05% Tween; (2) 0.01 N NaOH in 0.05% Tween; and (3) 100 mM TRIS-HCl, pH 7.5 in 150 mM NaCl in 0.05% Tween

↓

Add alkaline phosphatase conjugated antibody to the reporter oligonucleotide; 30 μl per well in 100 mM TRIS-HCl, pH 7.5, 150 mM NaCl, 0.5% dry milk and 0.05% Tween

↓

Incubate plates for 30 min at room temperature for antibody binding to the reporter

↓

Wash the plate with 100 mM TRIS-HCl, pH 7.5, 150 mM NaCl in 0.05% Tween to remove unbound antibody

↓

Add substrate

↓

Read plate for appropriate colormetric, chemiluminescent, or fluorescent product

Genomic sequences required to begin this assay can be amplified by a number of different methods, including LCR, 3SR, and PCR. We have used PCR amplification to obtain DNA targets listed on the following Table VI for litigation assay primers:

TABLE VI

(sequences of amplification primer sets)

Target Gene	Amplification Primers
β-globin	CAACTTCATCCACGTTCACCTTGCC AGGGCAGGAGCCAGGGCTGGGG
alpha$_1$-antitrypsin	TCAGCCTTACAACGTGTCTCTGCTT GTATGGCCTCTAAAAACATGGCCCC
cystic fibrosis	CAGTGGAAGAATGGCATTCTGTT GGCATGCTTTGATGACGCTTCTG

DNA amplification was performed using 5 μl of DNA (2 ng/μl for genomic DNA or 5 μl of treated material from an alternative source) is mixed with a pair of primer oligonucleotides (0.5 μM each) specific for the region of DNA to be amplified in a PCR buffer containing 0.05 U/μl of Taq polymerase, 50 mM KCl, 25 mM Tris HCl buffer at pH 8.3, 10 mM $MgCl_2$, 200 μg/ml gelatin, 0.1% Triton X-100, and 1.5 mM each of dATP, dCTP, dGTP and dTTP. The sample was overlaid with 60 μl of light mineral oil, denatured at 93° C. for 5 min target, and subjected to 40 cycles consisting of 20 sec at 93° C., 40 sec at 55° C., and 1 min at 72° C. Following temperature cycling, the sample was subjected to 10 min at 72° C. to complete extension of the DNA sample.

Oligonucleotides are synthesized and modified for particular functions in the ligation assay. The assay requires a minimum of two modified oligonucleotides. One oligonucleotide has a hook that permits capture of the oligonucleotide following ligation. An example of this is a biotinylated oligonucleotide which can be captured on streptavidin or avidin supports. The other oligonucleotide has a reporter group which, in the case of a fluorophore reporter, multiple reporters with different emission spectra could easily be incorporated into a single assay.

For an ELISA based system, probes which discriminate allelic forms of a gene are synthesized with a 5' biotin group. Reporter probes are enzymatically or chemically 5'-phosphorylated and labelled with the hapten digoxigenin. The hapten is added to the 3' end of the reporter probe by tailing 500 pM of oligonucleotide at 37° C. for 1 hour in 10 mM potassium cacodylate, pH 7.0, 1 mM $CoCl_2$, 0.1 mM DTT, 5 nM of digoxigenin dUTP, 0.05 μM of dATP, and 100 units of the enzyme terminal transferase in a total volume of 20 μl. After labelling, 2 μl of 3 M sodium acetate and 1 μl of yeast t-RNA (1 mg/ml) and 60 μl of 95% ethanol is added. The oligonucleotide is precipitated at 4° C. for 5 min and then collected by centrifugation at 6500×g for 5 minutes. The pellet is resuspended in 20 μl of distilled water and the process repeated. This precipitation removes unconjugated excess digoxigenin from the labelled probe. Example of oligonucleotides which discriminate alleles for three pathologic states are given in the following table VII:

TABLE VII

(sequences of example oligonucleotides for ELISA detection)

Target Gene	Form of Gene Detected	Biotinylated Primer	Labelled (L) Primer
β-globin	β^A	B1-ATGGTGCACCTGACTCCTGA	
			GGAGAAGTCTGCCGTTACTG
	β^S	B2-ATGGTGCACCTGACTCCTGT	
alpha $_1$ anti-trypsin	M	B1-GGCTGTGCTGACCATCGACG	
			AGAAAGGGACTGAAGCTGCT
	Z	B2-GGCTGTGCTGACCATCGACA	
cystic fibrosis	non-508	B1-ATTAAAGAAAATATCATCTT	
			TGGTGTTTCCTATGATGAAT
	508	B2-ACCATTAAAGAAAATATCAT	

Utilizing the procedure contained in the previous flow chart, a number of experiments were run and, after color development, data were obtained spectrometrically at a wavelength of 490 mN. Typical results for such tests have been tabulated in the following table VIII:

TABLE VIII

(spectrophotometric data from automated ligation reactions using Taq ligase)

Amplified Genomic DNA Target From:	Ligation Primer Mix B1 + L	Ligation Primer Mix B2 + L
β-globin		
β^A	1.27 ± 0.06	0.01 ± 0.01
β^S	0.04 ± 0.03	1.85 ± 0.03
$alpha_1$-antitrypsin		
M	1.85 ± 0.15	0.03 ± 0.01
Z	0.03 ± 0.03	1.47 ± 0.07
cystic fibrosis:		
non-508	1.33 ± 0.20	0.02 ± 0.01
508	0.01 ± 0.01	1.66 ± 0.16

Comparable levels of detection were achieved with either **T4** or Taq ligase. In addition, a number of ligation reactions have been performed for several other disease associated polymorphisms with comparable results. Additionally, eight different polymorphisms in the human T cell receptor loci have been examined with similar detection results. The present invention, therefore, appears to be generally applicable in the analysis of DNA polymorphisms consisting of single base substitutions, DNA deletion or insertions, or DNA translations.

In addition, a number of alkaline phosphatase substrates can be employed in the ELISA assay of the present invention including sensitive chemiluminescent substrates (10 attomole detection). The format of the assay is easily adapted to other reporter formats such as fluoropores which can be read in the appropriate microtiter format. Incorporation of the appropriate fluorophore format would, for example, permit multiplex analysis by ligation. In this scheme, oligonucleotides discriminating different alleles and/or different genes could be evaluated in a single assay. Furthermore, it is also possible that tandem ligation assays (ligation of oligonucleotides in chains) could be employed to assess closely spaced DNA polymorphisms such as those which exist in the major histocompatibility complex genes. Such modifications to the assay specifically depicted above are considered to be well within the scope of the present invention

The present invention can be used in a wide variety of DNA diagnostic screening. For example, and not intending to limit the scope of the present invention, such DNA diagnostic screens may include those according to the following summary:

A—INFECTIOUS DISEASES:

1. Viral Diseases: HIV, EBV, HPV, HSV, CMV, Hepatitis (non-A, non-B)
    - (i) blood and tissue screening
    - (ii) rapid identification
    - (iii) distinguish chronic infection from past exposure
    - (iv) distinguish resistant strains in mixed infection
2. Bacterial Diseases: Mycobacteria, Syphilis, Clamydia, Legionella, Campylobacter; Pneumonocystis, Lysteria, Lyme, Leprosy
    - (i) rapid identification of slow growing microbes
    - (ii) identification in immuno-deficient patients
    - (iii) testing food for contamination
3. Parasitic Diseases: Malaria, Trypanosomes, Leishmania
    - (i) rapid identification of "third world" blood diseases
    - (ii) screening travelers and armed forces

B—GENETIC DISEASES:

1. Single Allele Diseases: Cystic Fibrosis, Duchenne's muscular dystrophy, Sickle Cell Anemia, β-thalasemia, Haemophilia A, Gaucher, Tay-Sachs, Alsheimer's, Neurofibromatosis
2. Cancer: Retinoblastoma, Wilms tumor, Colon, Breast, Oncogenes, Tumor supressors
3. Multiple Allele Diseases: Coronary heart disease, Diabetes, High blood pressure, Schizophrenia, Manic-depression, Alcohol abuse
    - (i) predisposition to disease
    - (ii) preventive medicine, exercise, diet
    - (iii) genetic screening and counseling
    - (iv) gene therapy.

C—GENETIC IDENTIFICATION:

1. Humans: HLA typing, forensics
    - (i) tissue transplantation
    - (ii) genetic linkage analysis
    - (iii) human genome program
    - (iv) positive identification of missing children
2. Animals: Horses, Dairy cows, Cattle, Domestic pets
    - (i) pure genetic characteristics
    - (ii) confirm breeding lineage
    - (iii) positive identification of animals
3. Plants: Seed Stock
    - (i) assure genetic diversity
    - (ii) identify strains resistant to drought and disease

Thus, while we have illustrated and described the preferred embodiment of our invention, it is to be understood that this invention is capable of variation and modification, and we therefore do not wish to be limited to the precise terms set forth, but desire to avail ourselves of such changes and alterations which may be made for adapting the invention to various usages and conditions. Accordingly, such changes and alterations are properly intended to be within the full range of equivalents, and therefore within the purview of the following claims.

Having thus described our invention and the manner and a process of making and using it in such full, clear, concise and exact terms so as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same;

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 39

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGGAATAGG GGATGCGCCC CTAGTCCAAG GGAAAGTATA GCCCAAGGTA CACTAGGGCC 60

ATGACCCTGG AAGAGGCGAG GAAGCGGGTA AACGAGTTAC GGGACCTCAT CCGCTACCAC 120

AACTACCGCT ACTACGTCCT GGCGGACCCG GAGATCTCCG ACGCCGAGTA CGACCGGCTT 180

CTTAGGGAGC TCAAGGAGCT TGAGGAGCGC TTCCCCGAGC TCAAAAGCCC GGACTCCCCC 240

ACCCTTCAGG TGGGGGCGAG GCCTTTGGAG GCCACCTTCC GCCCCGTCCG CCACCCCACC 300

CGCATGTACT CCTTGGACAA CGCCTTTAAC CTTGACGAGC TCAAGGCCTT TGAGGAGCGG 360

ATAGAACGGG CCCTGGGGCG GAAGGGCCCC TTCGCCTACA CCGTGGAGCA CAAGGTGGAC 420

GGGCTTTCCG TGAACCTCTA CTACGAGGAG GGGGTCCTGG TCTACGGGGC CACCGCCGGG 480

GACGGGGAGG TGGGGGAGGA GGTCACCCAG AACCTCCTCA CCATCCCCAC CATCCCGAGG 540

AGGCTCAAGG GGGTGCCGGA GCGCCTCGAG GTCCGGGGGG AGGTCTACAT GCCCATAGAG 600

GCCTTCCTCC GGCTCAACGA GGAGCTGGAG GAGCGGGGGG AGAGGATCTT CAAAAACCCT 660

AGGAATGCGG CGGCGGGTTC CTTAAGGCAA AAAGACCCCC GCATCACCGC CAAGCGGGGC 720

CTCAGGGCCA CCTTCTACGC CTTAGGGCTT GGGCTGGAGG AGGTGGAGAG GGAAGGGGTG 780

GCGACCCAGT TTGCCCTCCT CCACTGGCTC AAGGAAAAAG GCTTCCCCGT GGAGCACGGC 840

TACGCCCGGG CCGTGGGGGC GGAAGGGGTG GAGGCGGTCT ACCAGGACTG GCTCAAGAAG 900

CGGCGGGCGC TTCCCTTTGA GGCGGACGGG GTGGTGGTGA AGCTGGACGA GCTTGCCCTT 960

TGGCGGGAGC TCGGCTACAC CGCCCGCGCC CCCCGGTTCG CCATCGCCTA CAAGTTCCCC 1020

GCCGAGGAGA AGGAGACCCG GCTTTTGGAC GTGGTCTTCC AGGTGGGGCG CACCGGGCGG 1080

GTGACCCCCG TGGGGATCCT CGAGCCCGTC TTCCTAGAGG GCAGCGAGGT CTCCCGGGTC 1140

ACCCTGCACA ACGAGAGCTA CATAGAGGAG TTGGACATCC GCATCGGGGA CTGGGTTTTG 1200

GTGCACAAGG CGGGCGGGGT CATCCCCGAG GTCCTCCGGG TCCTCAAGGA GAGGCGCACG 1260

GGGGAGGAAA GGCCCATTCG CTGGCCCGAG ACCTGCCCCG AGTGCGGCCA CCGCCTCCTC 1320

AAGGAGGGGA AGGTCCACCG CTGCCCCAAC CCCTTGTGCC CCGCCAAGCG CTTTGAGGCC 1380

ATCCGCCACT TCGCCTCCCG CAAGGCCATG GACATCCAGG GCCTGGGGGA AAAGCTCATT 1440

GAGAGGCTTT TGGAAAAGGG GCTGGTCAAG GACGTGGCCG ACCTCTACCG CTTGAGAAAG 1500

GAAGACCTGG TGGGCCTGGA GCGCATGGGG GAGAAGAGCG CCCAAAACCT CCTCCGCGAG 1560

ATAGAGGAGA GCAAGAAAAG AGGCCTGGAG CGCCTCCTCT ACGCCTTGGG GCTTCCCGGG 1620

GTGGGGGAGG TCTTGGCCCG GAACCTGGCG GCCCGCTTCG GGAACATGGA CCGCCTCCTC 1680

GAGGCCAGCC TGGAGGAGCT CCTGGAGGTG GAGGAGGTGG GGGAGCTCAC GGCGAGGGCC 1740

ATCCTGGAGA CCTTGAAGGA CCCCGCCTTC CGCGACCTGG TACGGAGGCT CAAGGAGGCG 1800

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GGGGTGGAGA TGGAGGCCAA GGAGAAGGGC GGGGAGGCCC TTAAAGGGCT CACCTCCGTG   1860

ATCACCGGGG AGCTTTCCCG CCCCCGGGAA GAGGTGAAGG CCCTCCTAAG GCGCCTCGGG   1920

GCCAAGGTGA CGGACTCCGT GAGCCGGAAG ACGAGCTACC TCGTGGTGGG GGAGAACCCG   1980

GGGGAGAACC CGGGGAGCAA GCTGGAGAAG GCCAGGGCCC TCGGGGTCCC CACCCTCACG   2040

GAGGAGGAGC TCTACCGGCT CCTGGAGGCG CGGACGGGGA AGAAGGCGGA GGAGCTCGTC   2100

TAAAGGCTTC C                                                        2111
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 676 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Thr Leu Glu Glu Ala Arg Lys Arg Val Asn Glu Leu Arg Asp Leu
1               5                   10                  15

Ile Arg Tyr His Asn Tyr Arg Tyr Tyr Val Leu Ala Asp Pro Glu Ile
            20                  25                  30

Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys Glu Leu Glu
        35                  40                  45

Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Leu Gln Val
    50                  55                  60

Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr
65                  70                  75                  80

Arg Met Tyr Ser Leu Asp Asn Ala Phe Asn Leu Asp Glu Leu Lys Ala
                85                  90                  95

Phe Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Ala
            100                 105                 110

Tyr Thr Val Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr
        115                 120                 125

Glu Glu Gly Val Leu Val Tyr Gly Ala Thr Arg Gly Asp Gly Glu Val
    130                 135                 140

Gly Glu Glu Val Thr Gln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg
145                 150                 155                 160

Arg Leu Lys Gly Val Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr
                165                 170                 175

Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg
            180                 185                 190

Gly Glu Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
        195                 200                 205

Arg Gln Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr
    210                 215                 220

Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Val Glu Arg Glu Gly Val
225                 230                 235                 240

Ala Thr Gln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Gly Phe Pro
                245                 250                 255

Val Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val Glu Ala
            260                 265                 270

Val Tyr Gln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro Phe Glu Ala
        275                 280                 285
```

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```
Asp Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu Trp Arg Glu Leu
    290                 295                 300

Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile Ala Tyr Lys Phe Pro
305                 310                 315                 320

Ala Glu Glu Lys Glu Thr Arg Leu Leu Asp Val Val Phe Gln Val Gly
                325                 330                 335

Arg Thr Gly Arg Val Thr Pro Val Gly Ile Leu Glu Pro Val Phe Leu
            340                 345                 350

Glu Gly Ser Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile
        355                 360                 365

Glu Glu Leu Asp Ile Arg Ile Gly Asp Trp Val Leu Val His Lys Ala
    370                 375                 380

Gly Gly Val Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr
385                 390                 395                 400

Gly Glu Glu Arg Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly
                405                 410                 415

His Arg Leu Leu Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu
            420                 425                 430

Cys Pro Ala Lys Arg Phe Glu Ala Ile Arg His Phe Ala Ser Arg Lys
        435                 440                 445

Ala Met Asp Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu
    450                 455                 460

Glu Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys
465                 470                 475                 480

Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln Asn
                485                 490                 495

Leu Leu Arg Gln Ile Glu Glu Ser Lys Lys Arg Gly Leu Glu Arg Leu
            500                 505                 510

Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn
        515                 520                 525

Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu Glu Ala Ser Leu
    530                 535                 540

Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu Leu Thr Ala Arg Ala
545                 550                 555                 560

Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe Arg Asp Leu Val Arg Arg
                565                 570                 575

Leu Lys Glu Ala Gly Val Glu Met Glu Ala Lys Glu Lys Gly Gly Glu
            580                 585                 590

Ala Leu Lys Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro
        595                 600                 605

Arg Glu Glu Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr
    610                 615                 620

Asp Ser Val Ser Arg Lys Thr Ser Tyr Leu Val Val Gly Glu Asn Pro
625                 630                 635                 640

Gly Ser Lys Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr
                645                 650                 655

Glu Glu Glu Leu Tyr Arg Leu Leu Glu Ala Arg Thr Gly Lys Lys Ala
            660                 665                 670

Glu Glu Leu Val
        675
```

(2) INFORMATION FOR SEQ ID NO:3:

-continued

```
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 7 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: Not Relevant
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

     Asp Ala Glu Tyr Asp Arg Leu
     1               5


(2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAYGCNGART AYGAYMGNYT                                                   20


(2) INFORMATION FOR SEQ ID NO:5:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCGGATAAC AATTTCACAC AGGA                                              24


(2) INFORMATION FOR SEQ ID NO:6:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 130 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA       60

CCATGATTAC GAATTTAATA CGACTCACTA TAGGGAATTC GAGCTCGGTA CCCCAAGGTA      120

CACTAGGGCC                                                             130


(2) INFORMATION FOR SEQ ID NO:7:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2051 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGACCCTGG AAGAGGCGAG GAAGCGGGTA AACGAGTTAC GGGACCTCAT CCGCTACCAC       60

AACTACCGCT ACTACGTCCT GGCGGACCCG GAGATCTCCG ACGCCGAGTA CGACCGGCTT      120
```

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```
CTTAGGGAGC TCAAGGAGCT TGAGGAGCGC TTCCCCGAGC TCAAAAGCCC GGACTCCCCC    180

ACCCTTCAGG TGGGGGCGAG GCCTTTGGAG GCCACCTTCC GCCCCGTCCG CCACCCCACC    240

CGCATGTACT CCTTGGACAA CGCCTTTAAC CTTGACGAGC TCAAGGCCTT TGAGGAGCGG    300

ATAGAACGGG CCCTGGGGCG GAAGGGCCCC TTCGCCTACA CCGTGGAGCA CAAGGTGGAC    360

GGGCTTTCCG TGAACCTCTA CTACGAGGAG GGGGTCCTGG TCTACGGGGC CACCGCCGGG    420

GACGGGGAGG TGGGGGAGGA GGTCACCCAG AACCTCCTCA CCATCCCCAC CATCCCGAGG    480

AGGCTCAAGG GGGTGCCGGA GCGCCTCGAG GTCCGGGGGG AGGTCTACAT GCCCATAGAG    540

GCCTTCCTCC GGCTCAACGA GGAGCTGGAG GAGCGGGGGG AGAGGATCTT CAAAAACCCT    600

AGGAATGCGG CGGCGGGTTC CTTAAGGCAA AAAGACCCCC GCATCACCGC CAAGCGGGGC    660

CTCAGGGCCA CCTTCTACGC CTTAGGGCTT GGGCTGGAGG AGGTGGAGAG GGAAGGGGTG    720

GCGACCCAGT TTGCCCTCCT CCACTGGCTC AAGGAAAAAG GCTTCCCCGT GGAGCACGGC    780

TACGCCCGGG CCGTGGGGGC GGAAGGGGTG GAGGCGGTCT ACCAGGACTG GCTCAAGAAG    840

CGGCGGGCGC TTCCCTTTGA GGCGGACGGG GTGGTGGTGA AGCTGGACGA GCTTGCCCTT    900

TGGCGGGAGC TCGGCTACAC CGCCCGCGCC CCCCGGTTCG CCATCGCCTA CAAGTTCCCC    960

GCCGAGGAGA AGGAGACCCG GCTTTTGGAC GTGGTCTTCC AGGTGGGGCG CACCGGGCGG   1020

GTGACCCCCG TGGGGATCCT CGAGCCCGTC TTCCTAGAGG GCAGCGAGGT CTCCCGGGTC   1080

ACCCTGCACA ACGAGAGCTA CATAGAGGAG TTGGACATCC GCATCGGGGA CTGGGTTTTG   1140

GTGCACAAGG CGGGCGGGGT CATCCCCGAG GTCCTCCGGG TCCTCAAGGA GAGGCGCACG   1200

GGGGAGGAAA GGCCCATTCG CTGGCCCGAG ACCTGCCCCG AGTGCGGCCA CCGCCTCCTC   1260

AAGGAGGGGA AGGTCCACCG CTGCCCCAAC CCCTTGTGCC CCGCCAAGCG CTTTGAGGCC   1320

ATCCGCCACT TCGCCTCCCG CAAGGCCATG GACATCCAGG GCCTGGGGGA AAAGCTCATT   1380

GAGAGGCTTT TGGAAAAGGG GCTGGTCAAG GACGTGGCCG ACCTCTACCG CTTGAGAAAG   1440

GAAGACCTGG TGGGCCTGGA GCGCATGGGG GAGAAGAGCG CCCAAAACCT CCTCCGCGAG   1500

ATAGAGGAGA GCAAGAAAAG AGGCCTGGAG CGCCTCCTCT ACGCCTTGGG GCTTCCCGGG   1560

GTGGGGGAGG TCTTGGCCCG GAACCTGGCG GCCCGCTTCG GGAACATGGA CCGCCTCCTC   1620

GAGGCCAGCC TGGAGGAGCT CCTGGAGGTG GAGGAGGTGG GGGAGCTCAC GGCGAGGGCC   1680

ATCCTGGAGA CCTTGAAGGA CCCCGCCTTC CGCGACCTGG TACGGAGGCT CAAGGAGGCG   1740

GGGGTGGAGA TGGAGGCCAA GGAGAAGGGC GGGGAGGCCC TTAAAGGGCT CACCTCCGTG   1800

ATCACCGGGG AGCTTTCCCG CCCCCGGGAA GAGGTGAAGG CCCTCCTAAG GCGCCTCGGG   1860

GCCAAGGTGA CGGACTCCGT GAGCCGGAAG ACGAGCTACC TCGTGGTGGG GGAGAACCCG   1920

GGGGAGAACC CGGGGAGCAA GCTGGAGAAG GCCAGGGCCC TCGGGGTCCC CACCCTCACG   1980

GAGGAGGAGC TCTACCGGCT CCTGGAGGCG CGGACGGGGA AGAAGGCGGA GGAGCTCGTC   2040

TAAAGGCTTC C                                                        2051
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 676 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: Not Relevant
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

-continued

```
Met Thr Leu Glu Glu Ala Arg Lys Arg Val Asn Glu Leu Arg Asp Leu
1               5                   10                  15

Ile Arg Tyr His Asn Tyr Arg Tyr Tyr Val Leu Ala Asp Pro Glu Ile
            20                  25                  30

Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys Glu Leu Glu
        35                  40                  45

Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Leu Gln Val
    50                  55                  60

Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr
65                  70                  75                  80

Arg Met Tyr Ser Leu Asp Asn Ala Phe Asn Leu Asp Glu Leu Lys Ala
                85                  90                  95

Phe Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Ala
            100                 105                 110

Tyr Thr Val Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr
        115                 120                 125

Glu Glu Gly Val Leu Val Tyr Gly Ala Thr Arg Gly Asp Gly Glu Val
    130                 135                 140

Gly Glu Glu Val Thr Gln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg
145                 150                 155                 160

Arg Leu Lys Gly Val Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr
                165                 170                 175

Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg
            180                 185                 190

Gly Glu Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
        195                 200                 205

Arg Gln Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr
    210                 215                 220

Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Val Glu Arg Glu Gly Val
225                 230                 235                 240

Ala Thr Gln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Gly Phe Pro
                245                 250                 255

Val Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val Glu Ala
            260                 265                 270

Val Tyr Gln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro Phe Glu Ala
        275                 280                 285

Asp Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu Trp Arg Glu Leu
    290                 295                 300

Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile Ala Tyr Lys Phe Pro
305                 310                 315                 320

Ala Glu Glu Lys Glu Thr Arg Leu Leu Asp Val Val Phe Gln Val Gly
                325                 330                 335

Arg Thr Gly Arg Val Thr Pro Val Gly Ile Leu Glu Pro Val Phe Leu
            340                 345                 350

Glu Gly Ser Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile
        355                 360                 365

Glu Glu Leu Asp Ile Arg Ile Gly Asp Trp Val Leu Val His Lys Ala
    370                 375                 380

Gly Gly Val Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr
385                 390                 395                 400

Gly Glu Glu Arg Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly
                405                 410                 415

His Arg Leu Leu Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu
```

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```
            420                 425                 430

Cys Pro Ala Lys Arg Phe Glu Ala Ile Arg His Phe Ala Ser Arg Lys
        435                 440                 445

Ala Met Asp Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu
    450                 455                 460

Glu Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys
465                 470                 475                 480

Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln Asn
                485                 490                 495

Leu Leu Arg Gln Ile Glu Glu Ser Lys Lys Arg Gly Leu Glu Arg Leu
            500                 505                 510

Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn
        515                 520                 525

Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu Glu Ala Ser Leu
    530                 535                 540

Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu Leu Thr Ala Arg Ala
545                 550                 555                 560

Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe Arg Asp Leu Val Arg Arg
                565                 570                 575

Leu Lys Glu Ala Gly Val Glu Met Glu Ala Lys Glu Lys Gly Gly Glu
            580                 585                 590

Ala Leu Lys Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro
        595                 600                 605

Arg Glu Glu Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr
    610                 615                 620

Asp Ser Val Ser Arg Lys Thr Ser Tyr Leu Val Val Gly Glu Asn Pro
625                 630                 635                 640

Gly Ser Lys Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr
                645                 650                 655

Glu Glu Glu Leu Tyr Arg Leu Leu Glu Ala Arg Thr Gly Lys Lys Ala
            660                 665                 670

Glu Glu Leu Val
        675
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CTGGCTTATC GAAATTAAT                                               19
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
CCAGGGTCAT TTTATTTTCT CCATGTACAA AT                                32
```

```
(2) INFORMATION FOR SEQ ID NO:11:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 33 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGGAGAAA ATAAAATGAC CCTGGAAGAG GCG                                   33


(2) INFORMATION FOR SEQ ID NO:12:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAGCCGGTCG TACTCGGC                                                    18


(2) INFORMATION FOR SEQ ID NO:13:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTTTTTCATG GTGCACCTGA CGCCTGG                                          27


(2) INFORMATION FOR SEQ ID NO:14:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTTCATGGT GCACCTGACG CCTCT                                            25


(2) INFORMATION FOR SEQ ID NO:15:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCATGGTGC ACCTGACGCC TCA                                              23


(2) INFORMATION FOR SEQ ID NO:16:
```

```
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 22 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAGAAGTCT GCCGTTACTG CC                                              22


(2) INFORMATION FOR SEQ ID NO:17:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 51 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACACCATGG TGCACCTGAC TCCTGAGGAG AAGTCTGCCG TTACTGCCCT G              51


(2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 51 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGTGGTACC ACGTGGACTG AGGACTCCTC TTCAGACGGC AATGACGGGA C              51


(2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 22 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGGTACCACG TGGACTGAGG AC                                              22


(2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 24 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCCTCTTCAG ACGGCAATGA CGTC                                            24


(2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 26 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
```

-continued

```
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACCTCTTCAG ACGGCAATCG CGTTTC                                            26


(2) INFORMATION FOR SEQ ID NO:22:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 28 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCTCTTCAG ACGGCAATCG CGTTTTTC                                          28


(2) INFORMATION FOR SEQ ID NO:23:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: Not Relevant
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

     Met Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu
     1               5                   10                  15


(2) INFORMATION FOR SEQ ID NO:24:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 15 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: Not Relevant
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

     Met Val His Leu Thr Pro Val Glu Lys Ser Ala Val Thr Ala Leu
     1               5                   10                  15


(2) INFORMATION FOR SEQ ID NO:25:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAACTTCATC CACGTTCACC TTGCC                                             25


(2) INFORMATION FOR SEQ ID NO:26:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 22 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
```

-continued

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGGCAGGAG CCAGGGCTGG GG 22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCAGCCTTAC AACGTGTCTC TGCTT 25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTATGGCCTC TAAAAACATG GCCCC 25

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGTGGAAGA ATGGCATTCT GTT 23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCATGCTTT GATGACGCTT CTG 23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

-continued

ATGGTGCACC TGACTCCTGA 20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGAGAAGTCT GCCGTTACTG 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGTGCACC TGACTCCTGT 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGCTGTGCTG ACCATCGACG 20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGAAAGGGAC TGAAGCTGCT 20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGCTGTGCTG ACCATCGACA 20

(2) INFORMATION FOR SEQ ID NO:37:

-continued

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     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTAAAGAAA ATATCATCTT                                      20


(2) INFORMATION FOR SEQ ID NO:38:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGGTGTTTCC TATGATGAAT                                      20


(2) INFORMATION FOR SEQ ID NO:39:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACCATTAAAG AAAATATCAT                                      20
```

We claim:

1. The cell line AK**76** designated as ATCC **55032**.

2. A plasmid selected from pDZ**1** and designated as ATCC **68307**, and pDZ**7** and designated as ATCC **68308**.

3. An expression vector comprising a DNA sequence encoding for a thermostable ligase selected from the group consisting of (1) *Thermus aquaticus* HB8 ligase; (2) a thermostable ligase having at least 6 sequential amino acid residues corresponding to 6 sequential amino acid residues in *Thermus aquaticus* HB**8** ligase; and (3) a ligase active mutant of *Thermus aquaticus* HB**8** ligase wherein an amino acid residue has been inserted, substituted or deleted in or from the amino acid sequence of the ligase.

4. An isolated nucleic acid molecule encoding a thermostable ligase enzyme, wherein the nucleic acid molecule is selected from the group consisting of:

the nucleic acid encoding the amino acid of SEQ. ID. No. 2;

the nucleic acid sequence set out in SEQ ID No. 1; and

nucleic acid molecules which hybridize under stringent conditions of 2×SSC, 40% formamide at 40° C. to the nucleic acid sequence set out in SEQ ID No. 1.

5. The isolated nucleic acid molecule according to claim **4**, wherein the isolated nucleic acid molecule has the nucleic acid sequence set out in SEQ ID No. 1.

6. The isolated nucleic acid molecule according to claim **4**, wherein the isolated nucleic acid molecule hybridizes under stringent conditions to the nucleic acid sequence set out in SEQ ID No. 1.

7. An expression vector comprising the nucleic acid molecule of claim **4**.

8. A host cell comprising the expression vector of claim **7**.

9. The host cell according to claim **8**, wherein the host cell is a bacterial cell.

10. The host cell according to claim **9**, wherein the bacterial cell is *Escherichia coli.*

11. A host cell comprising the isolated nucleic acid molecule according to claim **4**.

12. An isolated nucleic acid molecule comprising a nucleic acid sequence which hybridizes under stringent conditions of 2×SSC, 40% formamide at 40° C. to the nucleic acid sequence set out in SEQ. ID. No. 1 and wherein said nucleic acid molecule encodes a ligase enzyme which has a biological property of catalyzing the formation of a phosphodiester bond at the site of a single-stranded break in duplex DNA.

13. The isolated nucleic acid molecule according to claim **12**, wherein the thermostable *Thermus aquaticus* strain HB**8** ligase enzyme catalyzes the formation of a phosphodiester bond at the site of a single-stranded break in duplex DNA at temperatures between 50° C. to 90° C.

14. The isolated nucleic acid molecule according to claim **12**, wherein the thermostable *Thermus aquaticus* strain HB**8** ligase enzyme retains its catalytic activity when subjected to temperatures between 90° C. to 105° C.

15. An expression vector comprising the nucleic acid molecule of claim **12**.

16. A host cell comprising the expression vector of claim **15**.

17. The host cell according to claim **16**, wherein the host cell is a bacterial cell.

18. The host cell according to claim **17**, wherein the bacterial cell is *Escherichia coli.*

19. A host cell comprising the isolated nucleic acid molecule according to claim **12**.

* * * * *